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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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AAW03757
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2000US-0240816P.
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17-OCT-2000;
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21-MAR-2001;
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ABP45310;
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 Abp45310 Human BLy
Adg96137 Single ch
Abp44982 Human BLy
Adg95809 Single ch
Abp44943 Human BLy
Adg95770 Single ch
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Aay05694 Multiple
Abg78212 Human Fv
Abg991903 Human ant
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Copyright (c) 1993 - 2005 Compugen Ltd
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E Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWF) super family and induces B cell furniture and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABPA3990-ABP4122B represent
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                                                                                                                                 novel antibodies that immunospecifically
                                                         Lymphocyte Stimulating polypeptides, nt of cancers and immune disorders.
Vaughan T, Hilbert D;
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Choi GH,
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                                                                                                                                   invention describes
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diagnosis and treatment
Barash SC,
                             WPI; 2002-114799/15
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the lymphocyte stimulator (BLyS). The BLyS gate has been mapped to chromosome 13934 and encodes a protein that is a member of the tumour chromosome 13934 and encodes a protein that is a member of the tumour chromosome 13934 and encodes both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable havy proliferation and differentiation. Specifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders such, these compositions are useful for identifying immune disorders as ALDS and proliferative disorders including myastchenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and cativities such as antirheumatic, antiathritis, infectious diseases cativities such as antirheumatic, antiathritis, on or propeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format changes intentive such as article, but was obtained in electronic format changes in the printed sequence of the printed in electronic format directely from WIPO at ftp.wipo.int/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                                                                                 antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple solerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel antibodies that immunospecifically bind to bymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have proliferatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS
                                                                                              90 ThralaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
                                                                                                                                                                                 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
                                                                                                                                                                                                                                                                     130 GlySerGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
                                                                                                                                                                                                                                                                                                                                         antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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               SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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2001US-0276248P.
2001US-0277379P.
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16-MAR-2001;
21-MAR-2001;
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and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (c.g. common variable immunodeficiency syndrome (BLDS)). ABB43990-ABB41228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatorid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain antibody that immunospecifically binds BLyS SeqID 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCG--
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proliferation and differentiation. Specifically, it refers to single chain antibody molecules (ecfews) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The fresher invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatorid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This antiinflammatory, antiasthmatic, antiallergic and cytostatic. This cinvention. NOTE: The sequence data for this padent did not form part of the princed specification, but was obtained in electronic format circulty from WIPO at ftp.wipo.int/published pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; manusosuppressive; immunostimulati; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-027379P.
25-MAY-2001; 2001US-0293499P.
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Best Local Similarity:
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ABP44943
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell confidence in man differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
                                                                          Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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             Hilbert
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Matches:
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           Barash SC,
                                            WPI; 2002-114799/15.
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               Ruben SM,
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                                                                                                                                                                                 This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1343 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single contain antibody molecules (ecfvs) derived, preferably, from the variable contain antibody molecules (ecfvs) derived, preferably, from the variable contains thereof, of either human, murine, rat or monkey BLyS. The heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The confirmation refers to the use of such antibodies in various methods contain invention and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various cutivities such as antirheumatic, antialergic and cytostatic. This collypeptide sequence is a single chain antibody that binds BLyS of the printed specification, but was obtained in electronic format of the printed specification, but was obtained in electronic format or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immunoglobulin; Ig; transgenic; non-human mammal;
inactivated endogenous Ig locus; B-cell development;
human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
production; antibody.
                                                                                                            stimulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATCAATCATGGGAAGCACCAACTACAACCGGTCCCTCAAGAGTCGGGCG----- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody that immunospecifically binds to a B lymphocyte stimu (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                      Ä
                                                      Hilbert
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Matches:
Conservative:
Mismatches:
Indels:
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                                                     Vaughan TJ,
                                                                                                                                                            Example 1; SEQ ID NO 954; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW62794 standard; peptide; 80 AA
                                                    Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTCAGGATATTAGCAGC 72
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                          (HUMA-) HUMAN GENOME SCI INC
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80.77$
76.92$
67.00$
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                                                    Barash SC,
                                                                              WPI; 2003-505530/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 253 AA;
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                                                     Ruben SM,
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transgenic Xenomice, created using the method of the invention. The prediction the describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin (Ig) locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus in miser constant region and regulatory and switch sequences, human J-H genes, and human V-H genes and an inserted human kappa light chain Ig locus comprising a human N-H genes and an inserted human kappa light chain Ig locus comprising a human kappa constant region, J-kappa genes, and human V-H genes and an inserted human kappa light chain Ig locus comprising a human kappa constant region, J-kappa genes, and V-kappa genes, inserted are chain Ig locus comprising a human kappa constant region, J-kappa genes, and V-kappa genes, inserted are selected to restore normal B-cell development in the mammal. The transgenic animals have a near complete human ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e-g. when exposed to human li-8, EGFR or TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic non-human mammals - having an inactivated immunoglobulin
locus and a near complete human immunoglobulin locus, used for production
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                                                                                                                                                                                                                                                                                                                                                  Green
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                                                                                                                                                                                                                                                                                                                                                  Klapholz S, Mendez M,
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Matches:
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                                                                                                                                                                                                                                                                                                                                                  Jakobovits A, Kucherlapati R,
                                                                                                                                     97WO-US023091
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74.07$
70.37$
66.00$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of human antibodies.
                                                                                                                                                                                                                                                                             (ABGE-) ABGENIX INC.
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Best Local Similarity:
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WO9824893-A2.
                                                                                                                             03-DEC-1997;
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                                                                11-JUN-1998.
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note= "replaces Gly
                     Location/Qualifiers
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          Homo sapiens
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The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, compled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                             GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCAAGAGTCGGGCGAGTCAG
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the development of demyelination in CNS of MS. The invention provides assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy
                                                                                                                                                                                                                                                                                                                                                                                                   Human Fv molecule hypervariable region related peptide #87.
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, Peretz T;
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                                                                                                                                                                                                                                                               Similarity:
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                                                                                                                                              Sequence 97 AA;
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                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a heavy chain variable region (VH) as predicted
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          B-cell clonality; RA gene; diagnosis; human.
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Levanon A;

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the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, larcoma, larcoma, larbhoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one
                                                                                                                                                                                                                                                                                                                              1 GARATCAATCATGGGAAGCACCAACTACAACCCGTCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                              metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; letkraemia, inflammatory disease; cardiovascular disease; mycacardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular
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Levanon A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plaksin D, Vogel T, Nimrod A,
Amit B, Kooperman L, Peretz T,
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119
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG91903 standard; protein; 97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-DEC-2000; 2000US-00751181.
29-DEC-2000; 2000US-0258948P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human antibody fragment #87
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74.07$
70.37$
66.00$
                                                                                                                                                                             0.00847
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Richter T,
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                                                                                                                                                                                                                                                                                                                                                                                                                           ---IleSer 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, and cancer.
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                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                              NOLAN463-1A.SEQ (1-81)
                                                                                                                                Sequence 97 AA;
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                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                              Alignment Scores:
Pred. No.:
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ABG91903
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antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, cell-matrix, platelet-matrix, platelet and/or cell-platelet adheaion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases, inflammatory diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type.
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                                                                                                                                                                                                                                                                        the invention
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                                                                                                                                                                                                                                                                                                    Sequence 97 AA;
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Best Local Similarit
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determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparing framework sequences between non-human and human antibodies. This sequence represents a human heavy chain variable region gene segment used in the
                              comprising making chimeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis for selection, for humanisation. The method is useful for making a humanised antibody or a converted antibody. The method is applicable for converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support non-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for direct comparison of framework sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody library, CD1 region, CD2 region, VH region, VL region, immunoglobulin, CD3 region, TM1 scFv; human.
                  invention describes a method of making a humanised antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein relating to the invention SEQ ID NO:55.
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97 AA;
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Pred. No.:
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Highly stable artificial antibody libraries with super-repertory and

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Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or
                                                                      The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a CDNA library as template for amplifying a fragment containing the CDI and CD2 regions of the VH or VL region of immunoglobulin gene and a fragment containing the CD3 region by PCR, respectively, producing VH and VL libraries, transferring into a host, and displaying the single-stranded antibody on a phage surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-cell; malignant; immunoglobulin; immunoglobulin variable region; Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; non-Hodgkin's lymphoma.
tool in
                proteomics and e.g. for diagnosis and treating various diseases
 contamination from unexpressible ones, useful as
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119
119
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Matches:
Conservative:
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                                              Page 101; 108pp; Japanese.
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                                                                                                                                                                                                                                                                Sequence 97 AA;
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                                     malignant or normal comprising: as menture to regardenting a sequence of a glycosylation site; and (c) classifying the cell as mentuoglobulin (1g) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site; and (d) treating a patient suffering from a risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor; and (3) screening for substances (S) capable of inhibiting the interaction between lectins of the type found in the germinal centre and N-glycosylation inhibitor. The method is useful in classifying a B-cell as glycosylation inhibitor. The method is useful in classifying a B-cell as malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence represents an Ig variable region sequence which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                             1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                            present invention describes a method for classifying a B-cell as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                             NOLAN463-1A.SEQ (1-81) x ADD28104 (1-97)
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          Disclosure; Fig 4; 61pp; English.
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29-MAY-2002; 2002US-0384197P.
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Best Local Similarity:
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                                                                                                                                                                                                                                  Sequence 97 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(8); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen blinding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody may be variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; stability; solubility; antigen binding affinity;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOLAN463-1A.SEQ (1-81) x ADF10048 (1-97)
Example 6; Fig 16a; 135pp; English.
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29-MAY-2002; 2002US-0384197P.
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Example 16; Fig 40a; 135pp; English.

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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected antibody caid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical properties of an antibody especially the stability, the physico-chemical properties of an antibody especially the stability, useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
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	97	19	-	<b>-</b>	9	0	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	
	0.00847	92.40	74.078	70.378	800.99	7	
Alignment scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	

NOLAN463-1A.SEQ (1-81) x ADF10150 (1-97)

61 GATATTAGC 69 |||||| ---IleSer 70 69 g 8 8 ò

Search completed: August 4, 2005, 18:14:24 Job time: 97.5 secs

Appl Appl Appl Appl Appl Appl Appl

Applayed App

Run

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Sequence 118, Application US/08545809A

Sequence 118, Application US/08545809A

Retent No. 6096878

GENERAL INFORMATION:

APPLICANT: Horido, Tasuku

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA
                                                                                             Sequence 1
Sequence 2
Sequence 4
Sequence 4
Sequence 2
                                        Sequence Sequence Sequence Sequence Sequence 1
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Sequence 4
Sequence 1
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            US-09-802-077-5
US-09-402-077-5
US-09-412-276-835
US-09-412-42-8-2
US-08-428-197-16
US-08-428-197-16
US-09-444-581-14
US-08-652-816A-14
US-08-652-816A-14
US-08-918-148-45
US-09-138-091A-45
US-08-918-148-45
US-08-918-148-45
US-08-918-148-45
US-08-918-148-19
US-09-490-153-65
US-09-471-276-880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: DCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPAN: 617-542-8906
TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-545-809A-92
US-08-767-128-18
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  Sequence 118, App
Sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 25, Appl
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Appli
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                                                                                       4, 2005, 18:05:28; Search time 23.25 Seconds (without alignments) 520.135 Million cell updates/sec
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                                                                                                                                                                       GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC 81
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1: /cgn2_6/prodateal/liaa/5A_COMB.pep:*
2: /cgn2_6/prodateal/liaa/5B_COMB.pep:*
3: /cgn2_6/prodatea/1/liaa/6A_COMB.pep:*
4: /cgn2_6/prodatea/1/liaa/6B_COMB.pep:*
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6: /cgn2_6/prodateal/liaa/backfiles1.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                 - protein search, using frame_plus_n2p model
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US-08-793-450-4
US-09-203-768A-2
US-08-393-450-8
US-09-372-425A-6
US-09-025-69B-25
US-09-490-070A-25
US-09-490-153-25
US-08-45-809A-137
US-08-545-809A-137
US-08-545-809A-137
US-08-545-809A-137
US-08-545-809A-137
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                                                                                                                                                                                                                                                                                 513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 2000000000
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Match Length
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; Sequence 8, Application US/08793450 ; Patent No. 6312690
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US-09-203-768A-2
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Best Local Similarity:
Query Match:
                                              Percent Similarity:
Best Local Similarity:
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Pred. No.:
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Pred. No.:
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US-08-793-450-8
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APPLICANT: EDELAMAN LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHABAIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: POSOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
STRATE: USA
ZIP: 22202
COMPUTER: USA
ZIP: 22202
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPATION
APPLICATION NUMBER: US/08/793,450
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F: RESTERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION NUMBER: 703-413-3300
TELEPHONEY/AGENT TO 3-2020
                                                                                                                                           116
119
11
11
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 4, Application US/08793450
Patent No. 6312690
; GENERAL INFORMATION:
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              SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                            92.40
74.07$
70.37$
66.00$
INFORMATION FOR SEQ ID NO:
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                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                            88 ---IleSer 89
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                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                             US-08-545-809A-118
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Genuence 2, Application US/09203768A
Patent No. 6787638
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Of Use
TITLE OF INVENTION: Of Use
TITLE REFERENCE: PLX 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 139
                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: MARGARITE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: KACZOREK, MICHEL
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
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119
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Conservative:
Mismatches:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                           Gaps:
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US-09-025-769B-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: DATE: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFFICATION: 536
PILING DATE: 03-MAR-1997
APPLICATION NUMBER: FR 94/10566
FILING DATE: D2-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHMAX: 703-413-3000
TELEFAX: 703-413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472
119
11
10
6
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09372425A
Patent No. 6475749
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOLAN463-1A.SEQ (1-81) x US-08-793-450-8 (1-472)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACMERSEE: Oppenherment wolls a Donner STREET: 2029 Century Park East, Suite CITY: Los Angeles STATE: CA COUNTRY: USA COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: FLORPY Disk COMPUTER: IBM PC compatible OPERALING SYSTEM: Windows 98 SOFTWARE: MS WORD CURRENT APPLICATION DATA: PELLICATION DATA: FILING DATE: August 11, 1999 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                        : 472 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.40
74.07$
70.37$
66.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-793-450-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-372-425A-6
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COMPUTER: Ploppy disk
SOFTWARE: PletentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: Ploppy disk
APPLICATION NUMBER: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION DATA: PSE-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILLING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: 1lag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
ITLE OF INVENTION:
Protein/(Poly) peptide libraries
ITLE OF INVENTION: Protein/(Poly) peptide libraries
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429
18
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Heavy chain without Tailpiece - AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOLAN463-1A.SEQ (1-81) x US-09-372-425A-6 (1-429)
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION UNBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELEPOMMUNICATION INFORMATION:
TELEPAX: (310) 788-5100
TELEFAX: (310) 788-5100
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHRACATERISTICS:
LENGTH: 429 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.0055487.40
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66.67$
62.43$
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GATATTAGC 69
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                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity:
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Alignment Scores:
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                                                                                                        Pred. No.:
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APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthuu, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & MoAuliffe
STREET: 1666 K. Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                        118
18
1
2
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-04n-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, EBq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                              NOLAN463-1A.SEQ (1-81) x US-09-025-769B-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ 1D NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acide
TYPE: amino acide
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20006
COMPUTER READABLE FORM:
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70.37%
66.67%
60.29%
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STATE: D.C.
COUNTRY: USA
                                                                                                                     TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                61 GATATTAGC 69
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Best Local Similarity:
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER TEADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patenit Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 14-Jan-2000

PRIOR APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INPORMATION: TEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION' Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                          118
18
1
2
6
6
                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                         NOLAN463-1A.SEQ (1-81) x US-09-490-070A-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                            Indels:
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLGGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 118 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                            0.00872
                                                                                                                                               84.40
70.37%
66.67%
60.29%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                   61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IleSer 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                            Sequence 137, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Maresda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
15
5
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Matches:
Conservative:
Mismatches:
Indels:
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ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/JP93/00603
FILING DATE: 10-MAY-1993
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOLAN463-1A.SEQ (1-81) x US-08-545-809A-137 (1-120)
                                                                                              GAAATCAATCATAGTGGAAGCACCAACTACAACCCG
                                                         NOLAN463-1A.SEQ (1-81) x US-09-490-324-25 (1-118)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REPEROKOCATORET NUMBER: 06501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEX: 200154
TELEX: 200154
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0248
81.00
79.17%
62.50%
57.86%
   60.29%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-545-809A-137
                                                                                                                                                                                               ---IleSer 70
                                                                                                                                                                    61 GATATTAGC 69
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                                                                                                                                                                                                                                                              US-08-545-809A-137
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   Query Match:
DB:
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                                                                                                                                                                                     1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                          50 GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: 970
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READBLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMBUTER: IBM PC compatible
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                     118
118
12
22
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                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: protein
) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00872
84.40
70.37%
66.67%
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70.37%
66.67%
60.29%
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                                                      Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Alignment Scores:
Pred. No.:
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                                                                                          Query Match
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APPLICANT: Dardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 5 SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOLAN463-1A.SEQ (1-81) x US-08-466-163B-5 (1-130)
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78
                       :::|||:::
92 AlaThrTyrTyrCysAlaTrpVal 99
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92 AlaThrTyrTyrCysAlaTrpVal 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 ----- AGCTGGTTA 78
-----AGCTGGTTA
                                                                                                                            Sequence 5, Application US/08466163B Patent No. 6329509 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-802-096-5; Sequence 5; Application US/09802096; Patent No. 6685339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 CAGGATATTAGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.028
80.70
47.92%
37.50%
57.64%
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Best Local Similarity:
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72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATURE SIEM: PC-DOS/MS-DOS SOFFWARE: Winbatin (Genetech)
CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/466,151
FILING DATE: 06-Jun-1995
RICASSIFICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 39/044
REFERENCE/DOCKET NUMBER: 39.044
REFERENCE/DAMINICATION: TELEPONE: 650/252-1489
                                                                                                                                            APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOLAN463-1A.SEQ (1-81) x US-08-466-151-5 (1-130)
                                                         S-08-466-151-5
Sequence 5, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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80.70
47.92%
37.50%
57.64%
89 SerValAspThr 92
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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Best Local Similarity:
Query Match:
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                                         RESULT 11
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Method of Preventing the Onset of Allergic Disorders (as amended. TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended. FILE REFERENCE: PO718P2CJUS
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-06-14
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
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PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
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Length:
Matches:
Conservative:
Mismatches:
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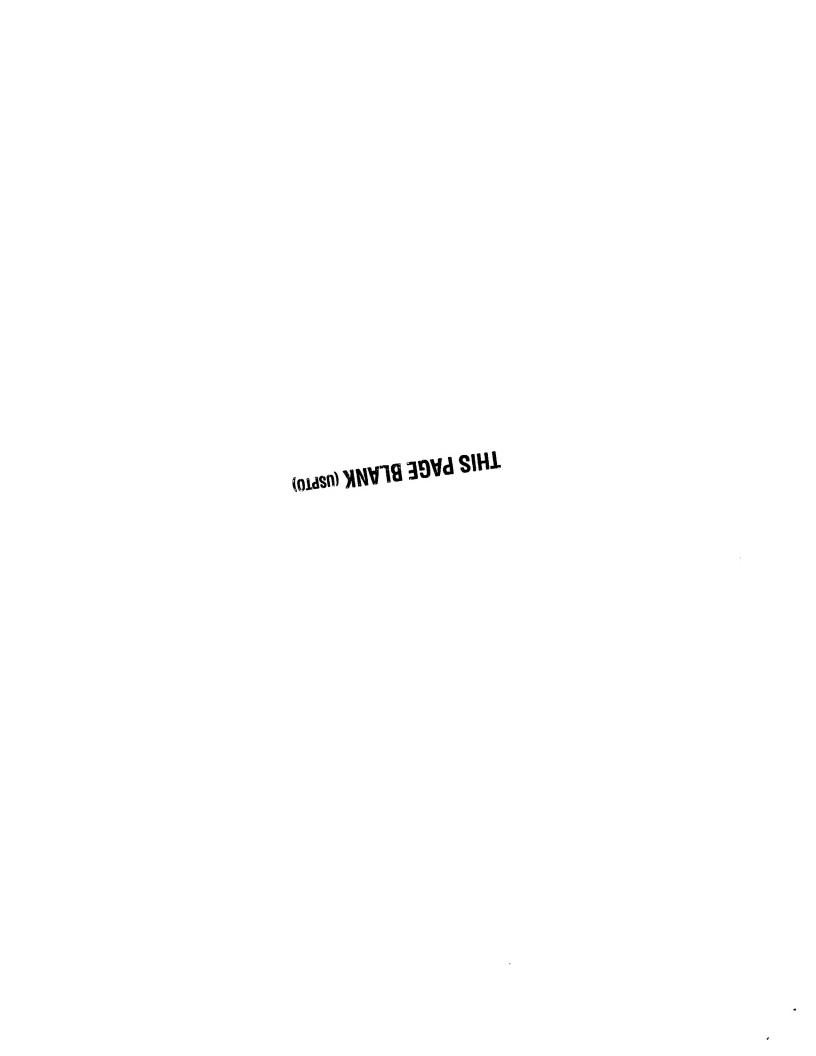
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72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
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; Sequence 5. Application US/09802077
; Sequence 5. Application US/09802077
; GENERAL INFORMATION:
    APPLICANT: Jardieu, Paula M.
    APPLICANT: Presta, Leonard G.
    TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
    FILE REFERENCE: P0718P2C2US
    CURRENT APPLICATION NUMBER: US/09/802,077
    CURRENT FILING DATE: 2001-03-08
    PRIOR FILING DATE: 1995-03-15
    PRIOR PLICATION NUMBER: US 08/405,617
    PRIOR PLICATION NUMBER: US 08/185,899
    PRIOR PLICATION NUMBER: US 07/85,995
    PRIOR PLICATION NUMBER: US 07/879,495
    PRIOR PLILING DATE: 1992-06-14
    PRIOR PLILING DATE: 1992-06-07
    PRIOR PLILING DATE: 1992-06-07
    PRIOR PLILING DATE: 1992-06-07
    PRIOR PLILING DATE: 1992-06-07
    PRIOR PLILING DATE: 1991-08-14
    NUMBER OF SEQ ID NOS: 64
    SEQ ID NOS: 64
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Matches:
Conservative:
Mismatches:
Indels:
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                                           TYPE: PRT
ORGANISM: Mus musculus
US-09-802-096-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5
; NUMBER OF SEQ ID NOS: ; SEQ ID NO 5
                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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                               LENGTH: 130
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Sequence 835, Application US/09471276

Sequence 835, Application US/09471276

Setent No. 6822072

GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PLIE REFERENCE: GENSET.025CP1
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT PILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER PILING DATE: 1998-04-09
EARLIER FILING DATE: 1999-04-28
EARLIER FILING DATE: 1999-04-28
EARLIER PILING DATE: 1999-04-28
EARLIER PILING DATE: 1999-04-28
SEALIER FILING DATE: 1999-04-28
SEALIER FILING DATE: 1999-04-28
SOFTWARE: Patent.pm
SEQ ID NOS: 1622
SEQ ID NOS: 1622
SEQ ID NOS: 1622
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Matches:
Conservative:
Mismatches:
Indels:
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92 AlaThrTyrTyrCy8AlaTrpVal 99
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79.40
66.67%
59.26%
56.71%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-09-471-276-835
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Perfect score:

Sequence:

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6 Run Scoring table:

Total number

Searched:

Minimum DB Maximum DB

Database

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Sequence 87, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 47, Appl
Sequence 118, Appl
Sequence 90, Appl
Sequence 90, Appl
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Sequence 1321, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 2001-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PAPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

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PRIOR APPLICATION NUMBER: 60/293,499
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0.05-09-864-761-92

0.05-09-965-76-192

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0.05-09-880-748-18-1333

0.05-09-880-748-18-1659

0.05-09-880-748-18-1659

0.05-09-880-748-1847
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SUMMARIES
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Match 1
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-G-/cgn2 1/USPTO-6pool PNOLANDR28463-1/runat 04082005 125809 24629/app_query.fasta_1.5-
-DB=Published Applications AA -QFMT=fastan -SUFFXX=rapb -MINNATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-ICPU=3 -NO MMAP -LARĞEQUERY.-NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                                                               2005, 18:20:25; Search time 80.25 Seconds (without alignments) 788.093 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PCT_REW PUB_CPp: *
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13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *
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15: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep: *
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17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
10: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOM
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFREENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-010-17
PRIOR PILING DATE: 2000-010-17
PRIOR PILING DATE: 2000-06-16
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Matches:
Conservative:
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113.10
20.63%
20.63%
80.79%
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1231
LENGTH: 249
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                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-880-748-1321
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US-10-898-408-12
; Sequence 12, Application US/10898408
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: GALLBERT, Laurent J.
; APPLICANT: PAN, Wei;
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Version 3.2
; SEQ ID NO 12
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Conservative:
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41.18%
37.25%
68.86%
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1321
; LENCTH: 249
; TYPE: PRT
; ORGANISM: Homo mapiens
US-10-293-418-1321
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ORGANISM: homo sapiens
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Best Local Similarity:
Query Match:
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Publication No. US20030059937A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver: 2.0

SEQ ID NO 993

LENGTH: 250
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Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT FILING DATE: 2002-11-27
FRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
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Matches:
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NOLAN463-1A.SEQ (1-81) x US-10-898-408-12 (1-115)
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CORGANISM: Homo sapiens
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US-09-880-748-954

Sequence 954, Application US/09880748

Publication No. US2030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITIE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/216,210

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-17

PRIOR PRIOR PRIOR DATE: 2001-03-17
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2000-10-17
PRIOR PELING DATE: 2000-10-17
PRIOR PILING DATE: 2000-16-17
PRIOR PILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 993
LENGTH: 250
TYPE: PRT
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70 SerGlnAspThrSerAsn 75
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Percent Similarity:
Best Local Similarity:
Query Match:
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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TITLE OF INVENTION: PLURAL Wh AND WE REGIONS AND ANTIBODIES PRODUCED
TITLE OF INVENTION: THEREPROM
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CURRENT APPLICATION UNMER: US/10/078,958
CURRENT FILING DATE: 1002-02-19
PRIOR FILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 79
SOFTWARE PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 80
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Matches:
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; Sequence 40, Application US/10194975
; Publication No. US20030038649A1
; GENERAL INFORMATION;
; APPLICANT: FOOCE, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FLLE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
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ORGANISM: Homo sapiens
US-10-078-958-2
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US-10-194-975-40
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GENERAL INFUGRATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: FF52P2

CURRENT PELICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-112-19

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-03-21

PRIOR PELING DATE: 2001-03-21

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2000-06-16

PRIOR PILING DATE: 2000-06-16
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                                               NOLAN463-1A.SEQ (1-81) x US-09-880-748-954 (1-253)
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Publication No. US20030070185A1
GENERAL INFORMATION:
APPLICANT: JAKOBOVITS, AYA
APPLICANT: KUCHERLAPATI, RAJU
APPLICANT: KALAHOLZ, SUSAN
APPLICANT: MENDEZ, MICHAEL J.
APPLICANT: GREEN, LARRY
                                                                                                                                                                                                                                                                ; Sequence 954, Application US/10293418; Publication No. US20030223996A1; GENERAL INFORMATION:
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70 SerGlnAspThrSerAsn 75
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70 SerGlnAspThrSerAsn 75
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CORGANISM: Homo sapiens
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US-10-078-958-2
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APPLICANT: BIO-TECHNOLOGY General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: (60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastESQ for Windows Version 3.0
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: X17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: X17-ISOLATED MOLECULES COMPRISING EPITOPES, AND USES THEREOF TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/032,423A CURRENT APPLICATION NUMBER: US/10/032,423A PRIOR APPLICATION NUMBER: 60/258,948 PRIOR PILING DATE: 12/29/2000 NUMBER OF SEQ ID NOS: 204 SOFTWARE: PASSES FOR WINDOWS VERSION 3.0
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                                                                       Sequence 87, Application US/10029988B; Publication No. US20040001839A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
       69 ---IleSer 70
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LENGTH: 97
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Publication No. US20040001822A1
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/44
CURRENT FILING DATE: 2001-12-31
FRIOR FILING DATE: 2001-12-39
NUMBER OF SEQ ID NOS: 204
SEQ ID NOS: 204
SEQ ID NO 87
LENGTH: 97
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US-10-308-817-83
Sequence 83, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Wu, Dayang
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
CURRENT APPLICATION UNMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 97
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ORGANISM: human
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US-10-032-037B-87
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Fublication No. US20040073011A1
GENERAL INFORMATION:
APPLICANT: HAGAY, et al.
TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 10793/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT FILING DATE: 2001-12-31
FRIOR APPLICATION NUMBER: 60/258,948
FRIOR PILING DATE: 12/29/2000
FRIOR FILING DATE: 12/29/2000
SPIOR FILING DATE: 12/29/2000
SPIOR FILING DATE: 12/29/2000
SPIOR FILING DATE: 12/29/2000
SOFTWARE: FastSEQ for Windows Version 3.0
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; ORGANISM: Homo sapiens
US-10-029-926B-87
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69 ---IleSer 70
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; ORGANISM: human
US-10-453-698-83
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US-10-029-926B-87
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US-10-453-698-83
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C.Species: Homo sapiens (man)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C.Date: 106-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C.Paccession: 837454
R.McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A.Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from proscription: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S;6805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Rur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
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                                                                                     A; Experimental source: V(H)4.2
C; Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.40
74.07$
70.37$
66.00$
A;Status: translation not shown
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                                                                    A;Cross-references: EMBL:X56364
                                                                                                                                                                                                                               0.00156
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74.07$
70.37$
66.00$
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Best Local Similarity:
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A,Molecule type: DNA
A,Residues: 1-97 <WEN>
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Best Local Similarity:
                     A; Molecule type: DNA
A; Residues: 1-97 <SAN>
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Pred. No.:
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R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.B.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Accession: 826898; S12420
R.Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A. Mol. Biol. 227, 776-799, 1992
A.Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: $26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-97 < TOM>
A; Residues: 1-97 < TOM>
A; Residues: 1-97 < TOM>
A; Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
A; Cross-references: Clone DP-63
B; Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: S09421; MUID:90059975; PMID:2511001
A; Recession: S12420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ileSerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 82
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                   Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78052; S23717 R;Harindranath, N. submitted to the EMBL Data Library, August 1990
                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 15-111 < HAW>
A; Cross-references: EMBL:X54441
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
21
241
141
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Matches:
Conservative:
Mismatches:
Indels:
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33.85%
32.31%
67.07%
                                                                                                                                                            A; Reference number: S78051
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A; Residues: 1-140 < HAR>
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S26898
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A,Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin A;Reference number: 847010
A;Recession: 847010
A;Accession: 847010
A;Status: prellminary
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Residues: 1-126 <MAH>
Cross-references: EMBL:235492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Jates: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C.Jates: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C.Jates: PS0341
R.Ratech, H.
R.Ratech, H.
B.Jochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A.Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
A.Reference number: PS0341; MUID:92171937; PMID:1540170
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C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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A, Molecule type: mRNA
A, Residues: 1-13 «RAT»
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
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Matches:
Conservative:
Mismatches:
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Gaps:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;58-74/Region: complementarity-determining F;75-106/Region: framework 3
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Best Local Similarity:
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Best Local Similarity:
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C) Species: Homo saptens (man)
C) Species: Homo saptens (man)
C) Species: Homo saptens (man)
C) Accession: JL0047
R) Hear, R.; Porster. A.; Lavenir, I.; Rabbitts, T.H.
C) Exp. Med. 167, 2011-2016, 1988
A; Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5
A; Reference number: JL0047
A; Molecule type: mRNA
A; Residues: 1-122 EARE>
A; Molecule type: mRNA
A; Residues: 1-122 EARE>
A; Note: the authors translated the reading frame which extends to the stop codon; the sequence belongs to the VH II subgroup
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology <IMM>
F; 23-105 / Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S47010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E. submitted to the EMBL Data Library, July 1994
A;Reference number: S37453
A;Accession: S37454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>A;Crose-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                  1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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Matches:
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92.40
74.07$
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74.07$
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---IleSer 48
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Best Local Similarity:
Query Match:
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Pred. No.:
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C,Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nuclectide sequences of eight human natural autoantibody V-H regions reveals app.
A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Recession: G34964
A;Rocession: G34966
A;Rocession: G34966
A;Rocession: G34966
C;Superfamences: UNIPROT: Q8WUX4; GB:M26998
C;Superfamenty: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
              Till Fabregion IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Balol, Chem. 266, 2836-2842, 1991
J. Balol, Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclo A;Reference number: A23746; WUID:91131575; PMID:1993660
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
                                                                                                                                                                                                                                                                                                   A;Molecule type: procein
A;Residues: 1-231 <LEO.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <LMM>
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Ig heavy chain V-IV region (Ab44) - human
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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Ig heavy chain V-IV region - human (fragment)
C;Species: Home Sapiens (man)
C;Species: Home Sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E; Kenter, M; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur B4; Timmers, E. Kenter, M; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur Bur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob A;Reference number: A49028
A;Retus: preliminary
A;Recession: B49028
A;Retus: preliminary
A;Retus: preliminary
A;Recession: B49028
A;Retus: preliminary
A;Retus
              Figrillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma Bur. J. Immunol. 22, 1781-1788, 1992

By Artitle. An anti-B cell aucoantibody from Wiskott-Aldrich syndrome which recognizes i blay Reference number: A49045; MUID:92324290; PMID:1623923

A; Reference number: A49045

A; Residues: preliminary

A; Residues: DAA

A; Residues: 1-140 <GRI>
A; Residues: Backbone (NCBIN:108088, NBIP:108089)

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: hetecotetramer; immunoglobulin

F; 34-116/Domain: immunoglobulin homology <IMM>
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C, Accession: A49045
R; Grillot-Courvalin, C.;
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C;Accession: S41114
R;Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the BWBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
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                                                                                                                                                                                                                            Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
                                   50 GlullelleHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---
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67.86%
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A; Accession: $44114
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-129 <HAW>
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Job time : 20.25 secs
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A; Roses-references: EMBL: Z12370; NID: 932960; PIDN: CAA78240.1; PID: 932961
A; Note: designated DP-70
R; Sanz, I: Kelly, P: Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: S09421; MUID: 90059975; PMID: Z511001
A; Accession: S12419
A; Accession: S12419
A; Residues: I-98 <SAN>
A; Cross-references: EMBL: X56363
A; Note: designated 4.19
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
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S14474
S14474
Ig heavy chain V region - human
Ig heavy chain V region - human
C;Species Home sapiens (man)
C;Species Home sapiens (man)
C;Accession: S14474
R;Van Bs. J. H.; Gamelign Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Accession: S14474
A;Accession: S14474
A;Accession: DNA
A;Residues: 1-97 <ESJ>
A;Cross-references: EMBL:X56591; NID:G37235; PIDN:CAA39929.1; PID:g1335354
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
C;Accession: S26905; S12419
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905
A;Status: preliminary
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69 49.3 116 1 HV61 MOUSE P18532 mus m 67.4 48.1 2348 2 Q82027 Q62027 anaba 66.9 47.8 476 2 Q6GMX1 Q6GMX1 P106 1 HV60 MOUSE P18531 mus m 65 46.4 116 1 HV60 MOUSE	65 46.4 478 2 QGNYH3 64 45.7 478 2 Q7Z379 60.8 43.4 3118 2 Q17575 59.5 42.5 1160 1 TFC3 YEAST 59.1 42.4 150 2 095973 59.1 39.7 274 2 Q9FL48	27         59         42.1         136         2         Q6LBQ5         Q6LBQ5           28         59         42.1         137         1         HV46         MOUSE         P01822           29         59         42.1         209         1         UPP         GCEIH         Q88m74           30         58.7         41.9         209         2         Q8XWUO         Q8xwu0	.3 451 2 Q6NGD8 Q6ngd8 .3 467 1 DPO4_CORGL Q8nnp4 .3 1083 1 KGB8_HUMAN Q9c0h5 .1 393 2 Q7WZ77 Q7WZ77 .1 963 2 Q8P5M2 Q8p5m2 .0 496 2 Q96KX8 Q96Kx8	57.2 40.9 729 1 DCMA MOOTH 57 38.3 337 2 Q6LOH3 57 40.7 1916 2 Q9VKG8 56.7 40.5 212 2 0926K5	56.6 40.4 360 2 Q92UL5 Q92UL5 Q92ul5 rhizobium 56.6 40.4 408 1 YBXO ARATH Q92q34 arabidops 56.4 40.3 390 2 Q6HH60 Q6Hh60 bacillus C6HH60 C6HH60 C6HH60 C6HH60 C6HH60 C6HH60 C6HH00 C6H10 C	56.4 40.3 588 2 Q813F9	ALIGNMENTS  RESULT 1  072376 1D 07237003 (TrEMBLrel. 25, Last endotate) 1D 01-077-2003 (TrEMBLrel. 25, Last sanotation update) 1D 02 Name-VH4-34 1D 02 Name-VH4-34 1D 03 Nority Natch: 66.004 1D 03 Nority Natch: 60.004 1D 03 Nority Natch: 116 1D 03 Nority Natch: 66.004 1D 03 Nority Natch: 66.004 1D 03 Nority Natch: 110	Oy 1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGGTCCCTCAAGAGTCGGGGGAGTCAG 60
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - protein search, using frame_plus_n2p model  Run on: August 4, 2005, 17:55:57; Search time 83.75 Seconds (without alignments) 990.529 Million cell updates/sec		Scoring table: BLOSUM62  Xgapop 10.0 , Xgapext 0.1  Ygapop 10.0 , Ygapoxt 0.1  Fgapop 6.0 , Fgapext 0.1  Delop 6.0 , Delext 0.1	Searched: 1612378 segs, 512079187 residues Total number of hits satisfying chosen parameters: 3224756	um DB seq length: 0 um DB seq length: 2000000000	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries	parameters: - n2p.model - DEV=x1p  SPTO model - DEV=x1p  START=1 - SUD=x1x=rup - MNNATCH=0.1 - L-COPCL=0 - L-COPCL=0  START=1 - SUD=x1x=rup - MNNATCH=0.1 - L-COPCL=0  START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - DETART=1 - SUD=x1x=x0000000  3728463-1 @CCN 1 1 305 @-MNLEN=0 - MAXLEN=20000000  3728463-1 @CCN 1 1 305 @-MNLEN=0 - MAXLEN=20000000  3728463-1 @CCN 1 1 305 @-MNLEN=0 - MAXLEN=20000000  3728463-1 @CCN 1 1 305 @-MNLEN=0 - LAGAPOP=10 - XGAPEXT=0  - YGAPOP=10 - YGAPEXT=0.1 - DELOP=6 - DELEXT=0.1  UniProt_03:*  UniProt_03:*  UniProt_03:*  UniProt_03:*  SUMMARIES  Query  ce Match Length DB ID  SUMMARIES  Query  derived by analysis of the total score distribution.  SUMMARIES  Query  derived by analysis of the total goore distribution.  SUMMARIES  Query  def. 0 595 2 QSBUX4  def. 0 597 2 QSBUX4  def	69.3 49.5 119 2 Q9UL/3 69.1 49.4 113 1 HV47_MOUSE F

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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG
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                            61 GATATTAGC
                                                                      ---IleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissue=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                      95
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                                                                                                                  RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toodhiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKenan F.J., McKernan K.J., Malke J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Johnshing M. Initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAPATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGGGAGTCAG 60
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AM19235.2; -.
PIN; (34364, 134964.)
HSSP; P01861; 1ADQ.
Ffam; PP07654; CI-set; 4.
SMART; SM00409; IG: 2.
SWART; SM00407; IGc1; 4.
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595 AA; 65290 MW; 0D4B50776545714E CRC64;
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119
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                           595 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOLAN463-1A.SEQ (1-81) x Q8WUX4 (1-595)
                                                                                                                                                                                                                            QBWUX4;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00426
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74.07%
70.37%
66.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
                                                                                                                                                                                                         PRELIMINARY;
                                                                      69
                                                                                                                                                                                                                                                                                                                     Hypothetical protein. Homo sapiens (Human).
                                                                                                                ---IleSer 70
                                                                      GATATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                         20
                                                                      61
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                                                                                                                                                                                                           OBWUX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                             RESULT 2
                                                                                                                                                                               ð
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TISSUB-Lymph;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.Z., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nitland M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

A Jones S.J., Marra M.A.;

and mouse C.DNA sequences.
                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073767; AAH73767.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65304 MW; 2A1E75F6AED85230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597
11
10
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
Gaps:
597 AA.
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
                                                            Created)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR003599; IG.
Interpro; IPR00310; IG-like.
Interpro; IPR003597; IG-like.
Interpro; IPR003596; IG-MHC.
INTERPRO; IRR00407; IG-1; 4.
SMART; SM00407; IG-1; 4.
SMART; SM00407; IG-1; 4.
                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein.
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74.07$
70.37$
66.00$
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aypothetical protein.
SEQUENCE 597 AA; (
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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IGHM protein. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[1] SEQUENCE FROM N.A.

NCBI\_TaxID=9606;

Last sequence update) Last annotation update)

Created) PRT;

01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,

625 AA

PRELIMINARY;

Q96AA6; **096AA6** 

69

61

---ileser 89 GATATTAGC

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RESULT 5
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                        87
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
IGHM protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01861; 1ADQ.
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1139
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1100
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                597 AA
                                                                                                                                                                                                PRT;
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InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig WHC.
Pfam; PP07654; Cl-set; 4.
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92.40
74.07%
70.37%
66.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                                                                                                                                                                PRELIMINARY;
                                                               61 GATATTAGC 69
                                                                                                        ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                        .69
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Straubberg R.L., Feingold B.A., Grouse L.H., Dorge J.G.,

Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Bosak S.A., McZwan P.J., McKernan R.J., Malke J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachay J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                  TISSUE-Lymph;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AAH17356.2; -.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSS0835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 625 AA; 68610 MW; P62FAB3ADE7ECBFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625
119
11
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; IG.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR00310; Ig-2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Pfam; PP07654; C1-eet; 4.
SMART; SM00407; IG2; 4.
SMART; SM00407; IG2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.00429
92.40
74.07%
70.37%
66.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissue=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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NOLAN463-1A.SEQ (1-81) x Q96AA6 (1-625)

1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 69 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

NOLAN463-1A.SEQ (1-81) x Q9BU10 (1-597)

Best Local Similarity:

Query Match:

Percent Similarity:

Score:

1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 8

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RESULT 7
                                                                                                        Q6P4I8
ID Q6
                                                                                                                                      셤
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

A thechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Hands F.F., Scheetz T.B.,

Brapleton M., Soarse M.B., Bonaldo M.F., Carainci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broaks S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gabbs R.A.,

Richards S., Worley K.C., Sodergren E.J., Lu X., Glibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Schwerkenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Cartywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Gones S.J., Marra M.A.,

"Mannan A. Mannan M. Mannan M
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO06180; AAH06180.1; -.
HSSP; P01061; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SEQUENCE 597 AA; 65300 MW; 2DĀFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597
118
22
6
                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                          597 AA
                                                                                                                                                          PRT;
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INICATPRO) IPRO03597; IG_C1.
INICATPRO) IPRO03066; IG_MHC.
INICATPRO) IPRO03596; IG_V.
Pfam; PF07654; C1-set; A.
                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17,
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86.40
70.37%
66.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                                                          PRELIMINARY;
                                                     69
                                                                                    ---IleSer 96
                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                     GATATTAGC
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissue=Muscle;
                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                      61
                                                                                                                                                          698088
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                                                                                                                      RESULT 6
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576
18
1
2
6
6
                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Conservative:
Mismatches:
Indels:
Gaps:
                                                                                 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                            Created)
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, BC063384; AAH63384.1; -...
HSSP; P01820; 1A7N.
InterPro; 1PR007110; 1g-1ike.
InterPro; 1PR003597; 1g_c1.
InterPro; 1PR003006; 1g_MHC.
InterPro; 1PR003596; 1g_WPC.
InterPro; 1PR003596; 1g_WPC.
InterPro; 1PR003596; 1g_W.
Pfam; PP00654; C1-8et; 2...
Pfam; PP0047; ig; 1...
SMART; SM00407; 1Gc1; 3...
SMART; SM00407; 1Gc1; 3...
                                                                                                         05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.40
70.37%
66.67%
60.29%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.0524
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Primary B-Cells;
69
                           83
                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 AA;
 61 GATATTAGC
                           ---Ileser
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                   IGHD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                   Name=IGHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                 Q6P4I8
Q6P4I8;
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NOLAN463-1A.SEQ (1-81) x Q6P4I8 (1-576)

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NOLAN463-1A.SEQ (1-81) x Q6GMX7 (1-477)
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SEQÜENCE
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90
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MAIschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

MISCHOLL S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

MARS S.F., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

M. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Maranche P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Moligher A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Mones S.J., Marra M.A.,

Mones S.J., Marra M.A.,

Mannan A., Scherst J., More than 15,000 full-length human
            GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA; 51631 MW; 9FE59C09C50CFF85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477
33
44
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                       477 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 477 AA; 51631 MW; 9FE59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC073765; AAH73765.1; ...
InterPro; IPR003199; Ig.
InterPro; IPR003109; Ig-like.
InterPro; IPR003509; Ig-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR03506; Ig_V.
Pfam; PF07654; C1-8et; Z.
Pfam; PF07654; C1-8et; Z.
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81.30
39.22%
33.33%
58.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSUE=Primary B-Cells;
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SM00407; IGc1; 3
SM00406; IGv; 1.
                                                                      ---IleSer 97
                                               GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Pred. No.:
                                                 61
                                                                      96
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                                                                                                                       Q6GMX7
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                                                                                               RESULT 8
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90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109
99 ----
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                                   70 GlulleAsnHisSerGlySerThrAsnTyrLysThrSerLeuLysSerArgValThr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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D segment.
J segment.
By similarity.
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17
1
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8D7FD52BB218171F
                                                                                                                                                                                                                                                                                                                                                                                                                   110 AlaValTyrTyrCy8AlaHi8GlySerSerTrp 120
                                                                                                                                                                                                                                                                                                                                       ----AGCAGCTGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
12-ULJ-1999 (Rel. 38, Last annotation update)
19 heavy chain V-II region ARH-77 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 AA.
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1. SMART; SM00406; IGV; 1. SMOSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal. SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ψ.
                                                                                                                                                                   64 ATT-----
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78.40
66.67%
62.96%
56.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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STRAIN=mix FVB/N; TISSUE=Mammary tumor; Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOLAN463-1A.SEQ (1-81) x Q99M22 (1-479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.08
72.60
33.93
30.36%
51.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OOGGMX6
AC DDT
OOG
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OOG DDT
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OOX MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 ValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=mix FVB/N; TISSUE=Mammary tumor; MEDLINE=22380257; PubMed=1247932; DOI=10.1073/pnas.242603899; MEDLINE=22380257; PubMed=1247932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butcow, E.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length CDNA clone CSODL004YN19 of B cells (Ramos cell line)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CAGGATATTAGCAGC
                                                                                                                                                                                                                                                                                                                                                                           TISSUE=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases EMBL; BX248300; CAD62627.1; -. HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7D1E2302410E4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
17
3
33
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOLAN463-1A.SEQ (1-81) x Q86SX2 (1-139)
                                                                                                                                                                           Homo sapiens (human) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 139 AA; 15573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR007110; Ig-like.
Interpro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE: PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein. Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.24
73.70
35.71%
30.36%
52.64%
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=B cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoaccope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                              Q86SX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  099M22
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099M2
AC 099M2
DD 001-JU
DT 01-JU
DT 0
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90 ArgAspThrSerLysAsnGlnPhePheLeuLysLeuAsnSerValThrThrGluAspThr 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brada S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richarda S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCA----
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TISSUB-Primary B-Cells;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (3M1-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
HSSP; D01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_mHC.
InterPro; IPR003596; Ig_w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||
| 110 AlaThrTyrTyrCysAlaSerArgGlyTyr----SerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GGATATTAGCAGCTGG 75
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22
44
34
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
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265ZI1
                    ID
DDT ACCOOC OOK SKE ACCOOC OOK SKE
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko, D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones C.D., Marra M.J.,
Jones C.D., Marra M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAGGATATTAGCAGC 72
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MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGHM protein.

Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCIL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH77766.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51083 MW; B3A9B7D0FDB1386E CRC64;
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13
3
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOLAN463-1A.SEQ (1-81) x Q6GMX6 (1-465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599; IG.
InterPro; IPR003109; IG-like.
InterPro; IPR003100; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-WHC.
InterPro; IPR003596; Ig v.
Pfam; PF007654; Cl-8et; 3.
Pfam; PF0047; ig; 4.
SWART; SW00409; IG; 2.
SWART; SW00407; IGC1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5
72.00
80.00%
65.00%
51.43%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 465 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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Pred. No.:
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1D 096EY
AC 096EY
DT 01-DE
DT 01-DE
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DT 01-DE
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Sacres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McEwran K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.W., Sodergens B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krayinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., R.
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TISSUB-Hybridoma;
MEDLINE=96211469; bubMed=8648670;
Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
"Targeting human immunodeficiency virus type 1 reverse transcriptase by intracellular expression of single-chain variable fragments to inhibit early stages of the viral life cycle.";
EMBL, U48716; AAB64342.1; --.
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
Mus musculus (Mouse).
Musmalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Straubberg R.;

Lubmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, BC01187; AAH11857.2; -.

REMBL, BC01187; AAH11857.2; -.

RISSP, P01820; 31530.

RICEPPO; IFR003599; IG.

RICEPPO; IFR003100; IG-like.

REMRT; SM00409; IG; 2.

RART; SM00407; IG-set; 4.

BR SMART; SM00407; IGG; 1.

BR SMART; BN00406; IGV; 1.

BR SNOSTE; PS50835; IG-LIKE; 5.

BR PROSITE; PS00290; IG MHC; UNKNOWN 3.
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113
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.61
72.00
80.00%
65.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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cal Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
GO:0003964; F:RNA-directed DNA polymerase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                           7DF20138E53865E4 CRC64;
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15
4
5
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16
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Matches:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF0335041; AAD56277.1; -.
PIR; PH0876; PH0876.
PIR; S12416; S12416.
HSSP; P01820; 1G70.
InterPro; IPR001710; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGV: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   119 AA.
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      InterPro; IPR003599; IG.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IGv; 2.
SMART; SM00406; IGv; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                               3.59
70.60
68.00%
64.00%
50.43%
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69.30
37.25%
29.41%
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119 AA;
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Best Local Similarity:
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Pred. No.:
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SEQUENCE
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Search completed: August 4, 2005, 18:20:06 Job time : 89.75 secs

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11   98.2   70.1   97 7   ADPIO048   Adfiloo48   VEGF anti-   12   98.2   70.1   97 7   ADPIO048   Adfiloo48   VEGF anti-   13   98.2   70.1   97 7   ADPIO049   Adfiloo50 Anti-body     14   98.2   70.1   114   3   AABO1923   Adfiloo50 Anti-loof     15   98.2   70.1   114   3   AABO1923   Adfiloo50 Anti-loof     16   98.2   70.1   114   3   AABO1923   AABO1925   AAFL-101     18   98.2   70.1   114   3   AABO1923   AABO1925   AABO1925	PN W0200202641-A1.  XX PV
Copyright (a) 1993 - 2005 Compagen Ltd.  OM nucleic - protein search, using frame_plus_n2p model Run on:  August 4, 2005, 17:55:32 ; Search time 92.5 Seconds Run on:  August 4, 2005, 17:55:32 ; Search time 92.5 Seconds Sequence:  1 CGGCGGAGTCAGGANATAGACAACCCGTCCCTCAAGAT 81 Scoring table BLOGNWS  Sequence:  Scoring table BLOGNWS  Sequence:  2 10:5522 seds, 386760381 residues Total number of htts satisfying chosen parameters:  Whimmum DB seq length: 00000000  Post-processing Whimum Match 100*  Maximum DB seq length: 00000000  Post-processing Whimum Match 100*  Listing first 45 summaries  Command line parameters:  ***COMMAND THE COMMAND TABLES - L'ANDACTH-0.1 - LOCOCCL-0 LOCOPEXT-0 LO	Result Querry B ID Description  1 100.1 71.5 25.3 5 ABP45322 Abp45322 Human BLy 2 100.1 71.5 25.3 7 ADG96149 Adg96149 Single ch 4 98.2 70.1 80 2 AAN62794 Aaw62794 Human ant 5 98.2 70.1 97 5 ABC91903 Adg961903 Human ant 6 98.2 70.1 97 5 ABC91903 Adg961903 Human ant 7 98.2 70.1 97 5 ABC91903 Adg961903 Human ant 8 98.2 70.1 97 6 ABC97107 Adg961903 Human ant 9 98.2 70.1 97 7 ADB75646 Human ger Add28104 Lymphoma

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diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP4399-ABP4728 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                    This invention describes novel antibodies that immunospecifically bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                    BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyGluSerPheSerGlyTyrTrrpSerTrp1leArgGlnProProGlyLysGlyLeu 45
                                                                                                                                                                                  B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomiatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in spicial samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune isorders and activity such as cancer, immune, and autoimmune isorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 TAGCAGCTGGTTAGCCGAAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain antibody that immunospecifically binds BLyS SeqID 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirtheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
Vaughan T, Hilbert D;
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Conservative:
Mismatches:
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Gaps:
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                                                                                                                                 Claim 1; Page 1993-1994; 3148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG96149 standard; protein; 253 AA.
Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.000635
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50.00%
47.73%
71.50%
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 Barash SC,
                                     WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sSer 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 253 AA;
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Best Local Similari
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Pred. No.:
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 Ruben SM,
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFv8) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysathenia and rheumatoid archritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and cotivities such as antirheumatic, antiallergic and cytostatic. This activities such as antirheumatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NoTE: The sequence data for this patent did not form part of directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                           Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human antibody 3H2 heavy chain amino acid sequence SEQ ID NO:118.
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Conservative:
Mismatches:
Indels:
                                                                                                                           Vaughan TJ,
                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 1333; 394pp; English
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                                                                                                                           Choi GH,
14-NOV-2002; 2002WO-US036496.
                                  16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                        (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                           Ruben SM, Barash SC,
                                                                                                                                                             WPI; 2003-505530/47.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA8927
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The present invention describes a protein comprising an immunoglobulin (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL) addomain. The protein binds a complex comprising a major histocompatibility complex (MHC) and a peptide, does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide comprising the novel protein and a carrier; (2) a cytotoxic T cell comprising one or more nucleic acids for expressing the Ig that binds a comprising one or more nucleic acids for expressing the Ig that binds a comprising one or more nucleic acids for expressing the Ig that binds a comprising one or more nucleic acids for expressing the Ig that bind the UC comprising an MHC and a peptide, and does not substantially bind the MHC in the absence of the MHC; (3) an isolated nucleic acid acid equence of the MHC; (3) an isolated nucleic acid comprising a first segment that encodes the Ig variable domain; (4) a comprising a first segment that encodes the protein; (5) a transgenic animal whose genome includes heterologus nucleic acid sequences that encode the protein; (6) identifying the protein; (6) identifying the corror an autigen-binding protein; (8) ablating or killing a target cell that card acids acids equences that encode the protein; (6) identifying the complex in a sample. A protein of the invention has cytostatic activity, and composition for treating or preventing a cancerous disorder in a subject; and (10) detecting an MHC-peptide composition for treating or preventing a composition for preventing an antibody which binds to an MHC-peptide complex where the peptide component in as peptide or an eursely and can an eursely and can an eursely and can an eursely and can an enterpressing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.
                     immunoglobulin; Ig; heavy chain variable domain;
light chain variable domain; major histocompatibility complex; MHC;
gpl00; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 28B; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (DYAX-) DYAX CORP.
(TECR ) TECHNION RES & DEV FOUND
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                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2002; 2002US-0358994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoogenboom HRJM, Reiter Y;
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                                                                                                                                                                                                                                   WO2003070752-A2.
                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                      Synthetic
                                                                                                        cancer.
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Sequence 125 AA;

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125
122
22
221
21
        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                         NOLAN463-1B.SEQ (1-81) x ADA89274 (1-125)
         000565
                  99.90
50.00%
47.83%
71.36%
                                       Best Local Similarity:
                           Percent Similarity:
Alignment Scores:
                                              Query Match:
DB:
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3 GGCGAGTCAGGATATTAGCAGC-----

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transgenic Xenomice, created using the method of the invention. The profication describes a transgenic non-human mammal which has genome specification describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin [Ig] locus, so that the mammal does not display normal B-cell development. The modifications also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus in micro constant region and regulatory and switch sequences, human J-H genes, and human N-H genes and an inserted human kappa [Ight chain Ig locus in germline configuration, the human X-rappa genes, human D-H genes, and human V-H genes and an inserted human kappa light chain Ig locus in germline noring constant region, J-kappa genes, including and V-kappa genes, where the number of V-H and V-kappa genes inserted are selected to restore normal B-cell development in the mammal. The call development in the mammal. The call development in the mammal. The customent of human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e.g. when exposed to human antibodies when exposed to particular antigens e.g. when exposed to human IL-B, EGFR or TNF- alpha the mice
                                                                                                                                                                                                                                                                                                                                Human, immunoglobulin, Ig, transgenic, non-human mammal,
inactivated endogenous Ig locus; B-cell development,
human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
production; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transgenic non-human mammals - having an inactivated immunoglobulin locus and a near complete human immunoglobulin locus, used for production of human antibodies.
               44 yLysGlyLeuGluTrplleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe
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19
3
                                                                                                                                                                                                                                                                                               Amino acid sequence of a human antibody fragment.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 71; 128pp; English.
                                                                                                                                                                                   AAW62794 standard; peptide; 80 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US023091.
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98.20
65.62%
59.38%
                                                                                                                                                                                                                                                          (first entry)
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                                                                                                        rLeuLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                       AAW62794;
25
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                                                                                                                                                                   AAW62794
                                                                                                                                              RESULT
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19-SEP-1997;
04-NOV-1997;
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                                                                                                                                                                               digestion
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                                                                                                Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
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   80 O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "replaces Glu of RA"
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                                                NOLAN463-1B.SEQ (1-81) x AAW62794 (1-80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                            ACAACCCGTCCCTCAAGAGT 81
                                                                                                                                                             AAY05694 standard; protein; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31. .66
/label= CDR2
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label= CDR1
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|abel= FR2
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/label= FR1
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 70.14%
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Region
Query Match:
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AAY 05
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This sequence represents a heavy chain variable region (VH) as predicted from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal from DNA of a multiple sclerosis (MS) patient. Sequences of VH of CSF B-cells were obtained from 4 MS patients (see AAX25316-19). Differences in nucleotide and predicted amino acid (see AAX25316-19). Differences compared with the closest known germline VH genes; for 4d76, this was RA. The results provided direct evidence that intrathecal clonally expanded B-cells from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that havd undergone antigen antibody-forming or memory lymphocytes that havd undergone antigen the development of demyelination in CNS of MS. The invention provides assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of B-cell clonality by amplification or enzymatic
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97CA-02216595.
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                                                                                                                                                                                                                     WPI; 1999-276985/23.
N-PSDB; AAX25318.
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nolan463-1b.seq.rag

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The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in sesociation with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferrably a cancer the medicament seminoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an cutte myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region
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|GlyLys----GlyLeu----GluTrp11eGlyGluI1eAsnH1sSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                     Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
                                                                                     Guy R, Lipschitz O, Szanton E, Levanon A;
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                                                                                                                                                                                                                                                             Claim 13; Page 193; 232pp; English
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                                                  (BIOT-) BIO-TECHNOLOGY GEN CORP
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65.62%
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                                                                                   Hagai Y, Lazarovits J,
Plaksin D, Peretz T;
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Best Local Similarity:
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infortant in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, inflammation, where the epitope is capable of being bound by an antibody, continuous antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune cellscape thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-rell-matrix, platelet-matrix, platelet of platelet and/or cell-platelet adhesion or aggregation, for increasing continuous or leukaemia cells to damage by anti-disease, anti-cancer or anti-cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases cancer, leukaemia, autoimmune diseases, inflammatory cellseases such as cancer, leukaemia, autoimmune diseases, inflammatory cellseases cancer, leukaemia, autoimmune diseases, inflammatory cellseases cancer, leukaemia, autoimmune diseases, inflammatory celusaemis chieseases such as myocardial infarction, cettinopathic diseases and other diseases mediated by abnormal platelet function and diseases and other diseases wediated by abnormal platelet function and diseases and other diseases wediated by abnormal platelet function and diseases and other diseases wediated by abnormal platelet function and diseases and other diseases wediated by abnormal platelet function and diseases and other diseases wediated by abnormal platelet function and diseases and other diseases wediated by abnormal platelet function and diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mar-Haim H;
Levanon A;
                                                                                                                                                                                                                                                                                               Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
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Peretz T,
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Amit B, Kooperman L,
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                                                                                                                                               (BIOT-) BIO-TECHNOLOGY GEN CORP.
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                                                                                 29-DEC-2000; 2000US-00751181.
29-DEC-2000; 2000US-0258948P.
                                          31-DEC-2001; 2001WO-US049442
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                                                                                                                                                                                       Hagai Y,
Richter T,
                                                                                                                                                                                                                                                       WPI; 2002-674776/72.
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04-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               comptising making chimeric antibodie marting a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibody in comparison to germline canonical CDR structure types of human antibody in comparison to converting a subject by a converted antibody or a converted antibody or a converted antibody or a converted antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for comparison of framework sequences in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody framework sequences between non-human and human antibodies. This sequence represents a human hash variable region gene segment used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                          Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
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Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR;
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                              canonical CDR structure type.
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                                                                                                                                                                                                                                                  Foote J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB75646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                              Homo
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The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a CDNA library as template for amplifying a fragment containing the CD1 and CD2 regions of the VH or VL region of immunoglobulin gene and a fragment containing the CD3 region by PCR, respectively, producing VH and VL libraries, transferring into a host, and displaying the single-stranded antibody on a phage surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Highly stable artificial antibody libraries with super-repertory and little contamination from unexpressible ones, useful as tool in proteomics and e.g. for diagnosis and treating various diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B-cell; malignant; immunoglobulin; immunoglobulin variable region;
                                            antibody library, CD1 region; CD2 region; VH region; VL region; immunoglobulin; CD3 region; TM1 scFv; human.
Human protein relating to the invention SEQ ID NO:55.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                        22-NOV-2002; 2002WO-JP012236.
                                                                                                                                                                                                                                                                                                                         22-NOV-2001; 2001JP-00358602
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                                                                                                                                                                                                                                                                                                                                                                                                                         Takayanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-449818/42
                                                                                                                                                                                                                                                                                                                                                                          (UYKE-) UNIV KEIO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                        WO2003044198-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                         Homo sapiens
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Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
                                                                                                                                                                                                                                                                                                    Computer optimization of physicochemical properties of comprises analyzing the interactions of amino acids at
                antibody heavy chain variable region VH_4-34.
                                                                                                                                                                                 01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                                                        03-MAR-2003; 2003WO-US006598
                                                                                                                                                                                                                                                  Lazar GA, Desjarlais JR,
                                                                                                                                                                                                                                                                           WPI; 2003-722066/68
                                                                                                        WO2003074679-A2.
                                                                                                                                                                                                                        (XENC-) XENCOR.
                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                 12-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97
                                                                                                                                                                                                                                                                                                                                positions.
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ID ADF1
    EXTXPX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (l) treating a patient suffering from or at risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor; and (3) screening for substances (5) capable of inhibiting the cinteraction between lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (5) has cytostatic activity, and can be used in gene therapy, and as a glycosylation inhibitor. The method is useful in classifying a B-cell as malignant or normal: The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence represents an Ig variable region sequence which is used in the cycentation of the present invention.
                                                                                                                                                                                                                                                                       Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 GlyLys----GlyLeu----GluTrplleGlyGlulleAsnHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; non-Hodgkin's lymphoma..
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                            (CANC-) CANCER RES TECHNOLOGY LTD
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                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 4; 61pp; English.
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                                                                                                                                                                    07-MAR-2002; 2002GB-00005395
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65.62%
59.38%
70.14%
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                                                                                                                                                                                                                                               WPI; 2003-902720/82.
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                                                                                        WO2003074059-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 97 AA
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                                                                Homo sapiens.
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                                                                                                                 12-SEP-2003
                                                    Synthetic
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variable

Marshall SA, Dahiyat B;

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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position (s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical property of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody way be variable region sequence used to illustrate the invention.
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Mismatches:
Indels:
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Matches:
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Example 6; Fig 16a; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF10150 standard; protein; 97 AA
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98.20
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variable region; human.
                      Homo sapiens.
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                                                                                                                                                                                                                               positions.
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                                                                                                                                                                                                                                                                                           The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method computases: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical properties of an antibody especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
          Antibody; stability; solubility; antigen binding affinity; variable region; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; stability; solubility; antigen binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                      variable region sequence used to illustrate the invention
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                     Desjarlais JR, Marshall SA,
                                                                                                                                                                                                                                                                        Example 16; Fig 40a; 135pp; English.
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29-MAY-2002; 2002US-0384197P.
                                                                                                          03-MAR-2003; 2003WO-US006598
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                                                                                                                                                                                                          WPI; 2003-722066/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                               WO2003074679-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97 AA;
                                                                                                                                                               (XENC-) XENCOR
                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                    12-SEP-2003
                                                                                                                                                                                                                                                    positions.
                                                                                                                                                                                     Lazar GA,
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DB:
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least noe antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 GlyLys----GlyLeu----GluTrplleGlyGluIleAsnHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nybrid antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                       Marshall SA,
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                                                                                                               03-MAR-2003; 2003WO-US006598
                                                                                                                                                                      01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
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Best Local Similarity:
WO2003074679-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97 AA;
                                                                                                                                                                                                                                                             (XENC-) XENCOR
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Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M, 1gM; V gene diversity; directed constitutive hypermutation; target sequence diversification; terminal deoxynucleotidyl transferase; TdT; clonal expansion; selection; heavy chain variable region; VH;

/note= "Encoded by CAG"

Location/Qualifiers

Key Misc-difference

WO200022111-A1

mutant; mutein.

sapiens

Ношо

Synthetic

Anti-Id1 Ab binding-defective mutant Ramos cell VH K70N/S77N

18-SEP-2000 (first entry)

AAB01949;

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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (1) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vi) comparing the sequence of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (vii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the selected framework sequences to one or more complementarity determining antibody fragment. The method is useful for producing a hybrid antibody fragment (claimed). The antibody and creamwork regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that mathain to receive the CDRs. This produces are that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the VH gene locus.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 83; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOLAN463-1B.SEQ (1-81) x ADJ80323 (1-97)
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                                                                                                                           03-DEC-2001; 2001US-0336591P.
                                                                                       03-DEC-2002; 2002WO-US038450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.000883
                                                                                                                                                             (ALEX-) ALEXION PHARM INC.
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65.62$
59.38$
70.14$
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Best Local Similarity:
Query Match:
DB:
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                 WO2003048321-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97 AA;
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                                                     12-JUN-2003
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Sale JE, Neuberger MS, Cumbers SJ;

(MEDI-) MEDICAL RES COUNCIL.

98GB-00022104. 99GB-00001141. 99GB-00013435.

99WO-GB003358

08-OCT-1999; 09-OCT-1998; 19-JAN-1999;

20-APR-2000

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The invention relates to a method of preparing a lymphoid cell line capable of directed constitutive hypermutation of a target nucleic acid region. The method comprises screening a cell population for ongoing target sequence diversification and selecting a cell in which the crate of target nucleic acid mutation exceeds that of other nucleic acid mutation of method for preparing a gene product with a desired activity, comprising expressing a nucleic acid encoding the target gene operably linked to a sequence which directs hypermutation e.g., terminal deoxynucleotidyl expressing a nucleic acid encoding the target gene operably linked to a sequence which directs hypermutation e.g., terminal deoxynucleotidyl cells which express a mutated gene product with the desired activity. One or more clonal populations of the identified cells is established, and cells with an improved activity of interest are selected. These steps may be iteratively repeated until a gene product with a desired of activity is obtained. The cell lines prepared according to the method of the invention are used for directed constitutive hypermutation of a nucleic cardiaced bypermutation of a gene product, preferably an enzyme or an immunoglobulin (Ig) with a desired activity. In the exemplifications of the invention, IgM-secreting Ramos cells were selected for use as they undergo hypermutation during clonal expansion. This was determined on the basis of the amount of diversity in the heavy chain variable region (VH). Sequences AAB01949-B01954 which have lost the ability to bind anti-idiotype antipodies (anti-idi have lost the ability to bind anti-idiotype antipodies (anti-idi Ab) relative to the wild-type VH (AAB01949). Note: The present sequence is not shown in the specification, but is derived from the wild-type Ramos cell VH shown in figure 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lymphoid cell line preparation useful for producing gene products having desired activity, involves screening and selecting cells having ongoing target sequence diversification and higher mutation rates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Page; 69pp; English
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N-PSDB; AAA52435.
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114

Alignment Scores: Pred. No.:

AAB01949 standard; protein; 114 AA

AAB01949 ID AAB0 XX

19	N	٣	80	0
Matches:	Conservative:	Mismatches:	Indels:	Gaps:
98.20	65.62%	59.38%	70.148	м
Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB;

NOLAN463-1B.SEQ (1-81) x AAB01949 (1-114)

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Search completed: August 4, 2005, 18:14:25 Job time: 93.5 secs

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9, App
Appli
Appl
                                                                                                                                                                                      Sequence 118, Application US/08545809A
Patent No. 6096878
CENERAL INFORMATION:
APPLICANT: Mateuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
COTTY: Boston
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                      US-09-372-425A-2
US-08-652-816A-13
US-08-918-148-79
US-08-138-091A-77
US-08-138-197-16
PCT-US93-10555-16
US-09-726-219A-169
US-09-726-219A-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: US
ZIN: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-193
ATTORNEY/AGSNT THYORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-545-809A-140
US-08-851-362D-22
                                                                                                                                                                                                                             US-09-802-077-7
US-09-025-769B-39
US-09-025-769B-65
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US-09-490-153-65
US-09-490-324-39
US-09-490-324-65
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US-08-466-163B-7
US-09-802-096-7
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US-08-325-955-6
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 TELERAX: 617-9
TELEX: 200154
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 -WODEL-frame+ nip.model -DEV=xlp
-WODEL-frame+ nip.model -DEV=xlp
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-G-Copi2 J/USPTO spool pyNoLAND8728463-1/runat 04082005 125807 24557/app_query.fasta_1.5
-DB=188ued Patents A. -OFMI-fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 25, Appl
Sequence 335, Appl
Sequence 335, Appl
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Sequence 4, Appli
                                                                                             4, 2005, 18:05:28; Search time 23.25 Seconds (without alignments) 520.135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 CGGGCGAGTCAGGATATTAG......ACAACCCGTCCCTCAAGAGT 81
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                    protein search, using frame_plus_n2p model
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US-08-793-450-4
US-09-203-768A-2
US-08-793-450-8
US-09-372-425A-6
US-09-490-070A-25
US-09-490-153-25
US-09-490-137-058-25
US-09-490-137-058-25
US-09-471-276-835
US-09-471-276-835
US-09-46-151-5
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                                                                                                                                                                                                                                                                                                    513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                       NOLAN463-1B.SEQ
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11.1
86.3
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Alignment Scores:
   Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08793450
; Sequence 4, Application US/08793450
; Patent No. 6312690
; Patent No. 6312690
; Patent No. 6312690
; APPLICANT: EDELMAN, LENA
APPLICANT: MARCARITTE, CHRISTEL
APPLICANT: CHAMBILI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES, 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: v.,
COUNTRY: USA
ZIP: 22.02
ZIP: 22.02
COMPUTER READABLE FORM:
COMPUTER: Ploppy disk
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 03-MAR-1997
CLASSIFICATION DATA:
PRILING DATE: 03-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REFERRANCE/DOCKET NUMBER: 660-118-0 PCT
FLECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                 116
119
2
3
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                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                    62 ACAACCCGTCCCTCAAGAGT 81
   118:
                                                                                                                                                 7.72e-05
98.20
65.62%
59.38%
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 123 amino acids
amino acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-793-450-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                 Alignment Scores:
Pred. No.:
                                  LENGTH:
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General Information US/09203768A

Patent No. 6787638

GENERAL INFORMATION:
APPLICANT: Huse, william D.
APPLICANT: Huse, william D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: of Use
TITLE OF INVENTION: of Use
TITLE OF INVENTION: of 1987
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT PILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 139
                                                                                                                                              RESULT 4
US-09-793-450-8
; Sequence 8, Application US/08793450
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
    APPLICANT: EDELMAN, LENA
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: MOCHEL
; APPLICANT: MOCHES
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
123
119
2
8
8
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119
23
8
                               Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Length:
Matches:
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Matches:
                                                                                                                    NOLAN463-1B.SEQ (1-81) x US-08-793-450-4 (1-123)
                                                                                                                                                                                                                    62 ACAACCCGTCCCTCAAGAGT 81
                                                                                                                                                                                                                                        62 ACAACCCGTCCCTCAAGAGT 81
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98.20
65.62%
59.38%
 7.89e-05
               98.20
65.62%
59.38%
70.14%
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                        Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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JS-09-025-769B-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: Patent Release #1.0, Version #1.30
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION NUMBER: P34/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INPORMATION:
NAME: PELENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/OCKET NUMBER: 24,618
REFERENCE CHARACTER NUMBER: 24,618
REFERENCE CHARACTER NUMBER: 24,618
RELEPHAN: 703-413-3200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTER SIN SEC ID NO: 8:
BENGTH: 472 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: AUTION acid
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Petent No. 6475749
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
APPLICANT: Ramon Montano
TITLE OF INVENTION: Improved Rh Antibody
CURBER OF SEQUENCES: 11
CURBER OF SEQUENCES: 1
CORRESEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: Windows 98 SOFTWARE: MS WORD CURRENT APPLICATION DATA: APPLICATION NDTA: RILING DATE: AUGUST 11, 1999 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ACAACCCGTCCCTCAAGAGT 81
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65.62%
59.38%
70.14%
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Best Local Similarity:
22202
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MEDITAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FBB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                   429
18
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Heavy chain without Tailpiece - AA
                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECHONE: (310) 788-500
TELEPAX: (310) 788-500
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
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Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ACAACCCGTCCCTCAAGAGT 81
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93.20
65.62%
56.25%
66.57%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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: USA
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS
                                                                                                                   US-09-490-070A-25
                                                                                                                                                    Alignment Scores:
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Sequence 25, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:
TIGHT No. 6696248

SECONDER NO. 6696248

TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe

STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
STATE: D.C.
COUNTY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                             Gaps:
              TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-7698-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 25
(212)596-9000
                                                                                                                                                                                                       0.000517
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50.00%
47.73%
65.79%
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Best Local Similarity:
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US-09-490-070A-25
TELEPHONE:
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                                                                                                                                                                                                         No.:
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                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: E 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
GENERAL INFORMATION:
Pack, Peter
I I I ag, Vic
Ge, Liming
Moroney, Simon
Plucekthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                             118
21
1
1
19
                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                     STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
RMATION FOR SEQ ID NO: 25:
LENGTH: 118 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                            3 GGCGAGTCAGGATATTAGCAGC
                                                                                                                                                                             0.000517
92.10
50.00%
47.73%
65.79%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10021
                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10021
ZIP: 10021
ZIP: 10021
ZIP: 10021
ZIP: 10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; Patent No. 6828422
; APPLICANT: Knappik, Achim
Pack, Peter
il July, vio Ce, Linding
Moroney, Simon
Plueckthun, Andreas
TITLE OP INVENTION: Protein/ (Poly) peptide libraries
; NUMBER OF SEQUENCES: 373
                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                         NOLAN463-1B.SEQ (1-81) x US-09-490-153-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                    Indels:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLGGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                              3 GGCGAGTCAGGATATTAGCAGC-----
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TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 118 amino acids
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                                                                                                                                                                        0.000517
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50.00%
47.73%
65.79%
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Query Match:
DB:
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64 sSer 65
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                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                 US-09-490-153-25
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                                                                                                                                                                                                                                                                                                                                                                                                  25 -----TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Horio, Taguku
APPLICANT: Horio, Taguku
APPLICANT: Matguda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOCLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: BOSTON
                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZUMPITER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: DISKETE CATION DATA: APPLICATION NUMBER: US/08/545,809A FILING DATE: 27-MAR-1996 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/JP93/00603 FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     3 GGCGAGTCAGGATATTAGCAGC------
                                                                                                                                                                                                                                                                                                                         NOLAN463-1B.SEQ (1-81) x US-09-490-324-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUTCATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPAX: 617-542-8906
                                                                                       25:
                                                                                                                                                                                                                                                                                   Gaps:
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 137, Application US/08545809A, Patent No. 6096878, GENERAL INFORMATION:
                                                                                                                                                                       0.000517
                                                                                                                                                                                           92.10
50.00%
47.73%
65.79%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-08-545-809A-137
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Query Match:
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                                                                                                                                                                                                                                                                                                                    gequence 835, Application US/09471276
| Patent No. 6822072 |
| GENERAL INFORMATION: |
| APPLICANT: Dumas Milne Edwards, J.B. |
| APPLICANT: Dumas Milne Edwards, J.B. |
| APPLICANT: Duclart A. |
| APPLICANT: Gordano, J.Y. |
| TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| Patent No. 6822072 |
| FILE REFERENCE: GENSET.025CP1 |
| CURRENT APPLICATION NUMBER: 09/09/471,276 |
| CURRENT FILING DATE: 1999-12-21 |
| EARLIER APPLICATION NUMBER: 09/057,719 |
| EARLIER PILING DATE: 1998-04-09 |
| EARLIER FILING DATE: 1998-04-09 |
| EARLIER FILING DATE: 1999-04-09 |
| SARLIER PILING DATE: 1998-04-09 |
| SOFTWARE: Patent.pm |
| SEQ ID NOS: 1622 |
| LERGICH: HAT
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US-08-466-151-5
; Sequence 5, Application US/08466151
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52.27%
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65.07%
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65.62%
50.00%
62.29%
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                       Percent Similarity:
Best Local Similarity:
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sSer 84
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US-09-471-276-835
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Alignment Scores:
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                                                               Query Match:
DB:
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Matches:
Conservative:
Mismatches:
Indels:
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STRTE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOLAN463-1B.SEQ (1-81) x US-08-466-151-5 (1-130)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA: 08/185899
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/879495
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFRX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Amino Acid
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40.74%
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Best Local Similarity:
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Pred. No.:
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Sequence 5, Application US/09802077
; Sequence 5, Application US/09802077
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Jeres, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR PILING DATE: 1994-01-26
; PRIOR PILING DATE: 1994-01-26
; PRIOR PILING DATE: 1992-06-14
; PRIOR PILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
                                                                                                                                                                                                                                                                                                                                                   |||::: ||| 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAgp 32
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Matches:
Conservative:
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                           Alignment Scores:
Pred. No.:
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    US-09-802-096-5
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended); FILE REFERENCE: P0718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT PILING DATE: 2001-03-08
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR PILING DATE: 1994-01-26
PRIOR PILING DATE: 1994-01-26
PRIOR FILING DATE: 1995-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Matches:
Conservative:
Mismatches:
Indels:
          Sequence 5, Application US/08466163B
Patent No. 6329509;
GENERAL INFORMATION:
APPLICANT: Dardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants FILE REFERENCE: P0718P2C101
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/466,163B
CURRENT FILING DATE: 1995-01-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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40.74%
31.48%
61.64%
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Best Local Similarity:
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JS-08-466-163B-5
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Total number Minimum DB E Maximum DB E

Searched:

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Sequence 128, App
Sequence 411, Appl
Sequence 401, Appl
Sequence 192, Appl
Sequence 192, Appl
Sequence 110, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 6, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 12, Appli
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Sequence 87,
Sequence 47,
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PESS.

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379
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Sequence E
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US-09-880-748-1333
                                                         Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/Cgn2_1/USPTO_spool_p/NOLAND8728463-1/runat_04082005_125809_24629/app_query.fasta_1.5
-Q=/Cgn2_1/USPTO_spool_p/NOLAND8728463-1/runat_04082005_125809_24629/app_query.fasta_1.5
-DB=Publiabhed_Applications_AA -QFMT=fastan -SUFPIX=rapb_-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITG=bits -STRAT=1 -EMDS=1. -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000
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-ICPU=3 NO MAAP -LAREGQUERY -NEG SCORES=6 "WAIT "DESPBLOCK=100 -LONGLOG
-DBY TIMEOUT=120 "WARN TIMEOUT=30" THREADS=1 -XGAPOF=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                                                                                                          August 4, 2005, 18:20:25; Search time 80.25 Seconds (without alignments) 788.093 Million cell updates/sec
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1 CGGCCGAGTCAGGATATTAG.....ACAACCCGTCCTCAAGAGT
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                   protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Database :

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| Sequence 1333, Application US/10293418
| Publication No. US20030223996A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| FILE REPRENCE: PF523P2
| CURRENT APPLICATION NUMBER: US/10/293,418
| CURRENT FILING DATE: 2002-11-27
| PRIOR APPLICATION NUMBER: 60/340,817
| PRIOR PILING DATE: 2001-11-16
| PRIOR FILING DATE: 2001-12-19
| PRIOR FILING DATE: 2001-06-15
| PRIOR FILING DATE: 2001-06-15
| PRIOR PLICATION NUMBER: 60/270,379
| PRIOR PLICATION NUMBER: 60/270,379
| PRIOR PLICATION NUMBER: 60/270,248
| PRIOR FILING DATE: 2001-03-21
| PRIOR FILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-01-17
| PRIOR FILING DATE: 2000-01-17
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEC ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 1333
LENGTH: 253
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47.73%
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, ORGANISM: Homo sapiens
US-10-293-418-1333
                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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26 GlyGluSerPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
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| US-1U-08-30-30-4
| US-2U-08-30-30-4
| Publication No. US20030070185A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: MCHERLAPATI, RAJU
| APPLICANT: MENDEZ, MICHAEL J.
| APPLICANT: MENDEZ, MICHAEL J.
| APPLICANT: GREEN, LARRY
| TITLE OF INVENTION: TRANSGENIC MAWMALS HAVING HUMAN IG LOCI INCLUDING
| TITLE OF INVENTION: TREBEROM
| TITLE OF INVENTION: TREBEROM
| FILE REFERENCE: CELL 4.18 CON
| CURRENT PELLING NUMBER: US/10/078,958
| CURRENT FILING DATE: 2002-02-19
| PRIOR APPLICATION NUMBER: 08/759,620
                                                                                                         18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA
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                                                                                                                                                                                                                                                                   US-10-371-942-118

Sequence 118, Application US/10371942

Publication No. US20030223994A1

GENERAL INFORMATION:
APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
APPLICANT: Reiter, Yoram

TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
FILE REFERENCE: 10280-034001

CURRENT APPLICATION NUMBER: US 60/358,994

PRIOR APPLICATION NUMBER: US 60/358,994

PRIOR PILING DATE: 2002-02-20

PRIOR PILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 121

SOFTWARE: FastSEQ for Windows Version 4.0
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22
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Matches:
Conservative:
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ORGANISM: Homo sapiens
JS-10-371-942-118
  3 GGCGAGTCA-
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Best Local Similarity:
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Pred. No.:
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LENGTH: 125
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TYPE: PRT
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| GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
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Conservative:
Mismatches:
Indels:
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Sequence 40, Application US/10194975

Publication No. US20030039649A1

GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REPERENCE: 501231.01

CURRENT APPLICATION NUMBER: US/10/194,975

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR PILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PATENTIN VEXBION 3.1

SEQ ID NO 40

LENGTH: 97
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                                                                                                                                                                                                                                                                                                                         62 ACAACCCGTCCCTCAAGAGT 81
PRIOR FILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 80
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                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-308-817-83
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SEQUENCE 87, Application US/10032037B
; Sequence 87, Application US/10032037B
; Sequence 87, Application US/10032037B
; Sequence 87, Application No. US20040001822A1
; Sequence 87, Application No. US20040001822A1
; TELE NECEDATION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIFTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR PILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SEQ ID NO 87
; LENTH: 97
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                                                                                                                                                                                                                                                                                                                                         NOLAN463-1B.SEQ (1-81) x US-10-308-817-83 (1-97)
; FILE REFERENCE: 1087-37; CURRENT APPLICATION NUMBER: US/10/308,817; CURRENT FILING DATE: 2002-12-03; NUMBER OF SEQ ID NOS: 195; SOFTWARE: Patentin version 3.1; SOFTWARE: Patentin version 3.1; LENGTH: 97; TYPE: PRT TYPE: PRT ORGANISM: human US-10-308-817-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 87, Application US/10029988B
; Publication No. US20040001839Al
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 yrAsnProSerLeuLysSer 65
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US-10-032-037B-87
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Pred. No.:
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Squence 87, Application US/10029926B
| Sequence 87, Application No. US20040073011A1
| GENERAL INFORMATION:
| APPLICANT: At AGAY, et al.
| TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
| FILE REFERENCE: 10793/50
| CURRENT APPLICATION NUMBER: US/10/029,926B
| CURRENT PILING DATE: 2001-12-31
| PRIOR FILING DATE: 12/29/2000
| NUMBER OF SEQ ID NOS: 203
| NUMBER OF SEQ ID NOS: 203
| SOFTWARE: FastSEQ for Mindows Version 3.0
| SEQ ID NO 87
| LENGTH: 97
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                       62 ACAACCCGTCCCTCAAGAGT 81
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US-10-032-423A-87
US-10-032-423A-87
Sequence 87, Application US/10032423A
GENERAL INFORMATION:
HEBBLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/45
CURRENT APPLICATION NUMBER: US/10/032,423A
CURRENT APPLICATION NUMBER: 60/258,948
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR PELING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 97
APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: X17-1SOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: X17-1SOLATED MOLECULES COMPRISING EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/46

CURRENT PELLING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR PILLING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 87

LENGTH: 97
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ORGANISM: Homo sapiens
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ORGANISM: homo sapiens
US-10-898-408-12
 Percent Similarity:
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APPLICANT: Sale, Julian E.
APPLICANT: Cumbers, Michael S.
APPLICANT: Cumbers, Sarah J.
TILLE OF INVENTION: Method of Generating Diversity
FILE REPRENCE: 18396/2002B
CURRENT APPLICATION NUMBER: US/10/733,532
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/GB02/02688
PRIOR FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 09/879,813
PRIOR FILING DATE: 2002-05-15
PRIOR PRILING DATE: 2002-05-15
PRIOR PRILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.2
SEQ ID NO 128
LENGTH: 114
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Matches:
Conservative:
Mismatches:
                       US-10-379-392-47

Sequence 47, Application US/10379392

Publication No. US20040110226A1

GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Debjarlais, John Rudolf
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILLE REPRENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT APPLICATION NUMBER: US 60/360,843
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR PILING DATE: 2002-03-01
PRIOR PRILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SOFTWARE: Patentin version 3.2

LENGTH: 97
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; Sequence 128, Application US/10733532
; Publication No. US20050026246A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-379-392-47
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ORGANISM: Homo sapiens
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Best Local Similarity:
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RESULT 15
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US-09-864-761-44315
Sequence 44315, Application US/09864761
Sequence 44315, Application US/09864761
Sequence 44315, Application US20020048763A1
Sequence 44315, Application US20020048763A1
Sequence 44315, Application US20020048763A1
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Sequence 44315, Application US20008864761
SEQUENCE Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TILE OF INVENTION: UNMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: US/09/632,366
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| Sequence 12, Application US/10898408
| Publication No. US20050058642A1
| GENERAL INFORMATION:
| APPLICANT: GALIBERT, Laurent J.
| APPLICANT: GALIBERT, Laurent J.
| TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
| FILE REFERENCE: 3467-A
| CURRENT PILING DATE: 2004-07-23
| PRIOR APPLICATION NUMBER: 6/490,027
| PRIOR FILING DATE: 2003-07-25
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 12
| LENGTH: 115
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GE 24263.6
PRIOR PALLY CANTON NUMBER: US 60/236,359
PRIOR PALLY CANTON NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PALLY CANTON NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PALLY CANTON NUMBER: PCT/USO1/00667
PRIOR PALLY CANTON NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00666
PRIOR PALLY CANTON NUMBER: PCT/USO1/00666
PRIOR PAPLICATION NUMBER: PCT/USO1/00666
PRIOR PAPLICATION NUMBER: PCT/USO1/00661
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Sequence:

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19 heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur-Rur; Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob A;Reference number: A49028; MUD:92008140; PMID:1915549
A;Accession: B49028
A;Status: preliminary
A;Residues: 1-143 <TIM>A;Residues: 1-143 <TIM>A;Residues: 1-143 <TIM>A;Residues: 1-143 <TIM>A;Residues: 1-143 <TIM>A;Residues: 1-143 <TIM>A;Residues: 1-143 <TIM
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A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
Ig heavy chain V r Ig heavy chain N r Ig heavy chain N r Ig gamma chain V r Ig heavy chain V r
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52.78%
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    Percent Similarity:
Best Local Similarity:
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                                                                  Alignment Scores:
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80.3
80.1
80.1
80.1
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-MODEL=frame+ n.DP. model - DEV=xlp
-Q=/cgn2 1/USFTO = DPO model - DFV = D
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heavy chain V r
heavy chain Vr
heavy chain Pre
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V-D
                                                                                                                                            4, 2005, 18:04:24 ; Search time 18:25 Seconds (without alignments) 854.089 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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(c) 1993 - 2005 Compugen Ltd
                                                                                                       protein search, using frame plus n2p model
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Maximum Match 100%
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S26805
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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                                                                                                                                                August
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Perfect score:
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Total number

Searched:

61 59

Score

Result Š. Database

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C.Species: Homo sapiens (man)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C.Accession: 837454
R.McIntcosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A.Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A.Reference number: 837453
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C;Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: $25,007.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: $25,007,MUID:92201299; PMID:1348029
                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377 C;Superfamily: immunoglobulin V reggion; immunoglobulin homology C;Koyerds: heterotetramer; immunoglobulin P:15-97/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross_references: EMBL:X75022; NID:9404311; PIDN:CAA52930.1; PID:9758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106
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Mismatches:
Indels:
                        Conservative:
Mismatches:
Indels:
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59.38%
70.14%
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>
                     Percent Similarity:
Best Local Similarity:
Query Match:
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A;Molecule type: DNA
A;Residues: 1-97 <WEN>
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Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (max)
C;Species: Homo sapiens (max)
C;Accession: $26898; $12420

R;Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Accession: $26895; MUID:93021117; PMID:1404388
A;Accession: $26895
A;Accession: $2685
A;Accession: $26895
A;Accession: $2685
A;Accession: $26895
A;Ac
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                                                S26805
Ig heavy chain V region - human
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens (man)
C;5pecies: Homo sapiens
A;7title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;7title: Polymorphism of human immunoglobulin N(H)4 germ-line genes.
A;7cose-references: EMBL: Z14241; NID: g377714; PIDN: CAA78610.1; PID: g1335376
C;5uperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
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A, Experimental source: V(H)4.2
C, Superfamily: immunoglobulin v region; immunoglobulin homology
C, Keywords: heteroterramer; immunoglobulin
F,15-97/Domain: immunoglobulin homology <IMM>
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Mismatches:
Indels:
Gaps:
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A; Residues: 1.140 kHRR.
A; Residues: 1.140 kHRR.
A; Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
A; Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
B; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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19 heavy chain V region (anti-B cell autoantibody) - human (fragment)

C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C; Accession: A49045

C; Accession: A49045

Bounch C; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma Bur., J. Immunol. 22, 1781-1788, 1992

A; Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                           53
                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
                                                                                                                                                                                                                           Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fil-14/Pomain: signal sequence (fragment) #status predicted <SIG>Fil5-140/Product: Ig heavy chain (fragment) #status predicted <MAT>F;29-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                    126
119
2
3
8
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Matches:
Conservative:
Mismatches:
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                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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A;Reference number: S78051
A;Accession: S78052
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A; Residues: 15-111 < HAW>
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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    Alignment Scores:
Pred. No.:
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Pred. No.:
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547010
19 heavy chain V4.21-UniqueD-J5 region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 847010
C;Accession: 847010
R;Manitted to the BMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
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Ig heavy chain V region precursor (clone cR18) - human

Ig heavy chain V region precursor (clone cR18) - human

C.Species: Hone sapiens (man)

C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996

C.Accession: JL0047

R.Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.

R.Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.

A.Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new A;Reference number: JL0047; MUID:88258392; PMID:3133445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Especial St. 1-122 - RABE>
A; Experimental source: T-cell line RPMI 8402
A; Experimental source: T-cell line RPMI 8402
A; Note: the authors translated the reading frame which extends to the stop codon; the A; Note: this sequence belongs to the VH II subgroup
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 23-105/ Domain: immunoglobulin homology < IMM>
                                                                                                                                                                61
                                                                                                                                                                                 20 GlyLys----GlyLeu----GluTrp11eGlyGlu1leAsnHisSerGlySerThrAsnT 37
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A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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Conservative:
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Conservative:
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Indels:
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C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
Limmunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals apply A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
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C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
C;Accession: S26905
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C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT
                                                                                 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin R;9-38/Region: framework 1 P;9-43/Region: complementarity-determining 1 P;44-57/Region: framework 2 P;58-74/Region: framework 2 P;58-74/Region: framework 3 P;75-106/Region: framework 3
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-97/Domain: immunoglobulin homology <IMM>
  A; Reference number: PS0341; MUID: 92171937; PMID: 1540170
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Conservative:
Mismatches:
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70.00%
                      A; Accession: PS0341
A; Molecule type: mRNA
A; Residues: 1-133 <RAT>
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Query Match:
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A; Residues: 1-97 <SAN>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B2346
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: B23346
A;Accession: B23346
A;Accession: B23346
A;Accession: B23346
A;Residues: 1-231 <LEO>
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(Species: Homo sapiens (man)
(S.Species: Homo-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
(S.Accession: PS0341
(S.Ratech, H.
Biochaen. Biophys. Res. Commun. 182, 1260-1263, 1992
A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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A;Accession: A49045
A;Etatus: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-140 cGRI>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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F;140-209/Domain: immunoglobulin homology <IMM>
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Pred. No.:
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133 17 1 0 0

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61 59

1 20 1

Conservative: Mismatches: Indels: Gaps:

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C,Accession: $14474
Syan Bs, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H
submitted to the EMBL Data Library, November 1990
A;Reference number: $14474
                                                                                                                                                                                                                                           42 GlyLys----GlyLeu----GluTrplleGlyGluIlelleHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C'Species: Homo sapiens (man)
C'Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
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                                                                                                                                                                                                  43 GlyGlySer----ileSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy
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Job time : 18.25 secs
                                                                                                                 NOLAN463-1B.SEQ (1-81) x S78055 (1-145)
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                                                                                                                                                          GGCGAGTCAGGATATTAGCAGC
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  Percent Similarity:
Best Local Similarity:
Query Match:
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A; Molecule type: DNA
A; Residues: 1-97 <ESJ>
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Best Local Similarity:
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A; Residues: 1-145 < HAR.>
A; Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
A; Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
B; Harindranath, N.; GGldfarb, I.S.; Ikematsu, H.; Burastero, S.B.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-98 «TOM»
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: destgnated DP-70
ENBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; WUID:90059975; PMID:2511001
A;Accession: S12419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 sGlyLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLe 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Homov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78055; S23720 R;Harindranath, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlySer----IleSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: mRNA
A, Cross-references: EMBL:X54445
A, Cross-references: EMBL:X54445
A, Note: the authors translated the codon GCA for residue 67 as Arg
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: immunoglobulin
F;1-1/Domain: signal sequence (fragment) #status predicted <SIG>
F;18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                        A;Note: designated 4.19
C;Superfantly: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Accession: S23720
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Matches:
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A;Reference number: S78051
A;Accession: S78055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                           A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-98 <SAN>
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uLysSer 66
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TISSUE-Hodgkin lymphoma;
Tinguel, W., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
Tinguel, W., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ564425; CAD92032.1; -.
EMBL, AJ564425; CAD92032.1; -.
InterPro; IRR007110; Ig-like.
InterPro; IRR007110; Ig-like.
InterPro; IRR003596; Ig_v.
SWART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                           Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
       Q9u173
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119
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Matches:
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Indels:
Gaps:
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                                                                                                                                                                                                                                    ALIGNMENTS
                            Q7Z379
HV47 MOUSE
Q99CA9
                                                                                                                                                          Q80632
Q6LBQ5
HV46 MOUSE
Q7ZB<del>B</del>2
                                                  061JQ4
090QV6
096KX8
06QJ60
06QJ62
                                                                                               090L43
09IUP1
09IUR6
07ZN97
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09J783
09IUT6
09IQS9
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Q9QKY2
Q9QKY3
Q698Z8
Q9UL73
Q6GMX1
              Q6NYH3
095973
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65.62%
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Homo sapiens (Human)
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Best Local Similarity:
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116 A
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                                               4, 2005, 17:55:57; Search time 83.75 Seconds (without alignments) 990.529 Million cell updates/sec
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                                                                                               81
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                                                                                             CGGGCGAGTCAGGATATTAG.....ACAACCCGTCCCTCAAGAGT
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Q9bqb8
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P06331
Q6gmx7
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Q99m22
P18532
Q6gmx6
Q65zi1
P18531
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Q9bu10
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                    protein search, using frame_plus_n2p model
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                                                                                                                                                          1612378 seqs, 512079187 residues
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Q8WUX4
Q6GWX5
Q9GU10
Q96AA6
Q9BQBB
Q9BQBB
Q6PX1
Q6GWX7
Q9GXX2
Q9GXX2
Q9GXX
Q99M22
HV61_MOUSE
Q6GXX6
Q65X11
HV61_MOUSE
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: uniprot sprot:*
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Q6GMX5;
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XX SIGNE-Lymph,

XX Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X3 Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X3 Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X4 Straubberg R.L., Feingold B.A., Grouse C.H., Schaefer C.F., Bhat N.K.,

X5 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X4 Hopkins R.F., Jordan H., Moore T., Max S.I., Wann J., Heibh F.,

X5 Lapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X6 Brownstein M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

X8 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X8 Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

X8 Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

X8 Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

X9 Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X9 Halton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

X8 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

X9 Jones S.J., Marra M.A.,

X1 "Generation and initial analysis of more than 15,000 full-length human
|||::: ||| GlyLys----GlyLeu----GluTrplleGlyGluIleAsnHisSerGlySerThrAsnT 59
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AAH19235.2; -.
EMBL; BC019245; AAH19235.2; -.
EMBL; BC019245; AAH19235.2; -.
EMBL; BC019245; G3464.
HSSP, P01861; 1ABO.
Pfam; PF07654; C1-set; 4.
SWART; SM00409; IGC; 2.
SWART; SM00400; IGC; 4.
SWART; SM00400; IGC; 4.
SWART; SM00400; IGC; 4.
SWART; SM00400; IGC; 4.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS508290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 protein.
595 AA; 65290 MW; 0D4B50776545714E CRC64;
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                                                                                                                                                                                                                                                               Created)
Last sequence update)
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                                                                                                   Ol-WAR-2004 (TERRELFEL 26, La 01-WAR-2004 (TERRELFEL 26, La Hypothetical protein. Homo sapiens (Human).
                                                                           ACAACCCGTCCCTCAAGAGT
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Best Local Similarity:
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A REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlausner R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Brotchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toodhyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Wachin T.B., Toodhyuki S., Carninci P., Frange C.,
RA Broak S.A., McKwam P.J., McKernan R.J., Mallek J.A., Gunaratne P.H.,
RA Bosak S.A., McKwam P.J., McKernan R.J., Mallek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Schwork M.J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Schward M.J.,
And Marra M.J.,
And Marra M.J.,
And M.J. Schmutz J., Myers R.M., Butterfield Y.S.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL, BCO73767; AA473767.1; -.
R InterPro; IPR001599; IG-1:
R InterPro; IPR001599; Ig-1ike.
R InterPro; IPR003597; Ig-1ike.
R InterPro; IPR003596; Ig-1ike.
R InterPro; IPR003596; Ig-1ike.
R InterPro; IPR003596; Ig-1ike.
R InterPro; IPR003596; Ig-1ike.
R SMART; SM00409; IG-1; 4.
R SMART; SM00409; IG-1; 4.
R SMART; SM00406; IG-1; 4.
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SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597
19
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3
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                                                                                                      Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                              05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last seques-JUL-2004 (TrEMBLrel. 27, Last annuly-thetical protein. Homo sapiens (Human).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOLAN463-1B.SEQ (1-81) x Q6GMX5 (1-597)
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98.20
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59.38%
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   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lymph;
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61

68 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 85 

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RESULT 5
                                                                 096AA6
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Braywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                   IGHM protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC002963; AAH02963.1; -. HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597
22
33
0
                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                597 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOLAN463-1B.SEQ (1-81) x Q9BU10 (1-597)
                                8
                                                    84
                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig WHC.
Pfam; PF07654; Cl-set; 4.
                                62 ACAACCCGTCCCTCAAGAGT
                                                                                                                   01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.000979
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65.62%
59.38%
70.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=Lymph;
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                                                     78
            61
                                                                                                           Q9BU10;
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DB:
                                                                                                Q9BU10
                                                                           RESULT 4
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TISSUB-Lymph;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Itschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Dosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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A Halton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchanko Y., Boutfard G.G.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rotiyuez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AAH17356.2;
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 625 AA; 68610 MW; P62PAB3ADE7ECBFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625
119
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                                                                                                                                                                                 Q96AA6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                             625 AA.
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                                                                                                                                                           PRT;
ACAACCGTCCCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P01861; IADO.
InterPro; IPR0031599; IG.
InterPro; IPR0031599; IG.
InterPro; IPR003006; IG_CI.
InterPro; IPR003006; IG_WHC.
InterPro; IPR003596; IG_V.
Pfam; PF07654; CI-Bet; 4.
SMART; SM00407; IG21; 4.
SMART; SM00407; IGC1; 4.
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65.62%
59.38%
70.14%
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                           IGHM protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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     62
                                                 78
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NOLAN463-1B.SEQ (1-81) x Q96AA6 (1-625)

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61

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Name=IGHD;
                  62
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                                                                                                                  Q6P4I8
                                                                                 RESULT 7
                                                                                                   Q6P4I8
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                                                                                                                                                                                                                                                                                                                                                          **X. **INSUERNULES**)**

**X. **MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**Altschul S.F., Zeeberg B., Buerdow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Zeeberg B., Buerdow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Zeeberg B., Buerdow K.H., Schaefer C.F., Bhat N.K.,

**A prichenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,

**A pricher M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

**Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Norley W. Touchman M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Norley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A.,

**A Radriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

**Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**A nones S.J., Marra M.A.;

**A manara M.A.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Strausberg R.;
L Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; GC06180; AAH06180.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003106; Ig-MC.
R InterPro; IPR003106; Ig-MC.
R InterPro; IPR003106; Ig-W.
R InterPro; IPR003106; Ig-W.
R EMBL; SNART; SNO0406; IG-V.
DR PROSITE; PS508315; IG-LIKE; 5.
DR PROSITE; PS00290; IG-MC; UNKNOWN 3.
SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597
118
2
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8
0
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                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                  597 AA.
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOLAN463-1B.SEQ (1-81) x Q9BQB8 (1-597)
                                                 62 ACAACCCGTCCCTCAAGAGT 81
                                                                    01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.20
62.50%
56.25%
65.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                 IGHM protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                 68
                                                                                 85
                                                                                                                                                  Q9BQB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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TISSUE=Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Itsueberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.L., Mang J., Halta F.F.,

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Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

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A Villalon D.K., Murxy D.M., Sodergran B.J., Lu X., Gibbs R.A.,

Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human

RT and mouse CDNA sequences.",

P. School P. Marra M.A.,

Proc. Natl. Acad. Sci. U.S.A. 99:16909-16903(2002).
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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FBB97C949D720F1E CRC64;
                                                                                           Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
576 AA
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INTERPRO; IPR001599; IG.

INTERPRO; IPR00110; IG-like.

INTERPRO; IPR003596; IG cl.

INTERPRO; IPR003066; IG w.

Pfam; PF007654; Cl-set; Z.

Pfam; PF00767; ig; l.

SWART; SW00409; IG; l.

SWART; SW00400; IG; l.

SWART; SW00400; IG; l.

FROSITE; PS00230; IG LIKE; 4.

PROSITE; PS00230; IG LIKE; 4.
                                                            Created)
PRT;
                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC063384; AAH63384.1;
HSSP; P01820; 1A7N.
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48.89%
46.67%
65.71%
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE=Primary B-Cells;
                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                               IGHD protein.
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NOLAN463-1B.SEQ (1-81) x Q6P418 (1-576)

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DB:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain V-II region ARH-77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16228 MW; 8D7FD52BB218171F CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
119 heavy chain V-II region ARH-77 precursor.
Homo sapiens (Human).
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D segment.
J segment.
By similarity.
                                                                                                                                                                                                       146 AA
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                                                                                                                                                                                                       PRT;
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87.20
59.38%
56.25%
62.29%
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115
146
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uLysSer 92
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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NON TER
SEQUENCE
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X TISSUB-PILMARY N.T.

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

R Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Townstein M.J., Usdin T.B., Toshiyuki S., Carninori P., Prange C.,

R Ana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Butfard G.G.,

Rodriguez A.C., Grimwood J., Schutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

on mouse CDNA sequences ";
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                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberger R:
Submitted (JUN 2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO73765; AA47765.1; -.
RINGERPO; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
RINGERPO; IPR003596; IG.
RINGERPO; IPR003596; IG.
R Pfam; PF00047; IG.
R Pfam; PF00047; IG.
R SMART; SM00409; IG; 4.
SMART; SM00409; IG; 4.
R SMART; SM00406; IGV; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS50835; IG_LIKE; 4.
R PROSITE; PS50835; IG_LIKE; 4.
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119
119
27, Created)27, Last sequence update)27, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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82.10
47.73
43.18
58.64
                         05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
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TISSUE-Primary B-Cells;
                                                                             Hypothetical protein.
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477 AA; 5
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                                                                                                                                                                                        NCBI_TaxID=9606;
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SEQUENCE 47
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SEQUENCE FROM N.A.
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Udel protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODLO04YM19 of B cells (Ramos cell line)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                           Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                               7D1E2302410E4F8C CRC64;
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2 2 4 4 4 9 9 9 9 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGCGAGTCAGGATATTAGCAGC------
                                      139 AA
                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             NOLAN463-1B.SEQ (1-81) x Q86SX2 (1-139)
                                                                                             Homo sapiens (human) (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                              SEQUENCE 139 AA; 15573 MW;
                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96EY0;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                          0.289
79.10
47.73%
43.18%
56.50%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                     PRELIMINARY;
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                 TISSUE=B cells;
Li W.B., Gruber C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 GAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 sSer 97
84
                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                 TISSUE=B cells;
BSer
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
83
                                               Q86SX2;
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                                      Q86SX2
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                   RESULT 10
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Rischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A histohul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Rohards S.A., McZwan P.J., McKernan K.J., Malek J.A., Gubs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ray Richards S.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and a standard and analysis of more than 15,000 full-length human and analysis of more than 15,000 full-length human and and analysis of more than 15,000 full-length human and analysis of more than 15,000 full-length human and and analysis of more than 15,000 full-length human and and analysis of more sold and analysis of sold and analysis of sold and analysis of sold and analysis of sold and analysis of sold and analysis of sold and analysis of sold and analysis of sold and analysis of sold and analysis o
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Buks musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                              MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hshelf F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Arboares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninoi P., Prange C.,
Ar Stapleton M., Soares M.B., Parameon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nillalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Willand A., Young A.C., Shevchenko Y., Bouffard G.G.,
Andring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
The Mouse CDNA sequences."
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31 LysProSerGinSerbeuSerbeuThrCysSerValThrGlyTyrSerlleThrSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAM-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
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SEQUENCE 479 Aa; 51992 MW; 768E39A138918892 CRC64;
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InterPro: IPR003597; Ig_ c1.
InterPro: IPR003595; Ig_ mHc.
InterPro: IPR003596; Ig_ wHc.
InterPro: IPR003596; Ig_ w.
Pfam; PP07654; C1-Bet; Z
SWART; SW00406; IGV, I.
PROSITE; PS00290; IG_ LIKE; 4.
PROSITE; PS00290; IG_ MHC; UNKNOWN_2.
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Best Local Similarity:
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Pred. No.:
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HV61_MOUSE
ID HV61_MC
AC P18532;
DT 01-NOV-
DT 25-OCT-
DE 19 heav
NAMES OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET 
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----AGCTGGTTAGC 32
                                                                                                                                             Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                         primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Framework-2.
Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 CGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 yTyr11eHisTyrSerGlyAsnThrSerTyrAsnProSerLeuLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region 1B43. Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13158 MW; 1CB547253681FF74 CRC64;
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16
5
3
13
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PDB; 1KCS; X-ray; H=19-116.
PDB; 1KCY, X-ray; H=19-116.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF000407; ig; 1.
SMART; SM00406; IGv. 1.
PR05TTE; PS50835; IG_LIKE; 1.
PR05TTE; PS50835; IG_LIKE; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOLAN463-1B.SEQ (1-81) x HV61_MOUSE (1-116)
                                                                                                                           MEDLINE=89279149; PubMed=2499654;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.805
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                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                          NCBI_TaxID=10090;
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                                                                                                                                                                  TISSUBERCE FROM N.A.

TISSUB-Primary B.Cells;

X REDLINE-2238825; PubMed=12477912; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Astapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Mochen P.J., McKernan K.J., Male J., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GlyLys----GlyLeu----GluTrpIleGlyArglleTyrThrSerGlySerThrAsnT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO73766, AAH73766.1; -.
InterPro; IPR003599; Ig. c1.
InterPro; IPR003599; Ig. c1.
InterPro; IPR0035906; Ig. MC.
InterPro; IPR003506; Ig. MC.
InterPro; IPR003506; Ig. WC.
InterPro; IPR003906; Ig. WC.
InterPro; IPR003906; Ig. A.
InterPro; IPR003904; Ig. 4.
InterPro; IPR00409; Ig. 4.
INTERPRO; IGC 1. Set; 3.
INTRT; SM00409; IGC; 2.
INTRT; SM00400; IGC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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20
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 yrAsnProSerLeuLysSer
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75.20
56.25%
50.00%
53.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
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TISSUE=Primary B-Cells;
                       Hypothetical protein. Homo sapiens (Human).
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Best Local Similarity:
                                                                                                                             NCBI_TaxID=9606;
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Q65211;
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Q65ZII
ID Q65ZII
AC Q65ZII
DDT READ BY SECOND BY SECO
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|178 SerGlyTyr-TrpAsnTrpIleArgLysPheProGlyAsnLysLeuAspTyrMetGlyTy 197
                                                                                                                                                                                                                                                                                                           TISSUE=Hybridoma;

WEDLINE=9611466; PubMed=8648670;

MEDLINE=9611466; PubMed=8648670;

MEDLINE=9611466; PubMed=8648670;

MEDLINE=9611466; PubMed=8648670;

Minhibit early stages of the viral life cycle.";

Tinhibit early stages of the viral life cycle.";

J. virol. 70:332-3400(1996).

EMBL; U48716; AAB64342.1; -.

RMEL; U48716; AAB64342.1; -.

RMEL; U48716; ABR003599; IG.

RICEPPO; IPR003599; IG.

RICEPPO; IPR003599; IG.

RICEPPO; IPR003599; IG.

RICEPPO; IRR003599; IG.

RICEPPO; IRR003599; IG.

RICEPPO; IRR0047; IG.

RMART; SM00409; IG.; 2.

SMART; SM00406; IGv; 2.

SMART; SM00406; IG.; 2.
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                                                                                                                             Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 rIleAsnTyrSerGlyAspThrTyrTyrAsnProSerLeuLy8Ser 212
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 -ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7DF20138E53865E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TCAGGATATTAGCAGCTGGTTAGCCGAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOLAN463-1B.SEQ (1-81) x Q65ZI1 (1-262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-directed DNA polymerase.
SEQUENCE 262 AA; 27842 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.19
72.80
55.56%
44.44%
52.00%
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                      NCBI_TaxID=10090;
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DB:
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Search completed: August 4, 2005, 18:20:08 Job time : 85.75 secs

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Anti-huma
Human mAb
Human ant
                                                    Human pho
Human pho
Human pho
Human leu
Human leu
Human ant
Human Fv
Human Fv
Human ant
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Human ant
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Antibody
Antibody
                                                                                                                                                                                                                                                                                                                                                Anti-huma
Anti-huma
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Anti-huma
                                                                                                                                                                                                                                                                                                                       Anti-huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human VH5
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-murine CTLA-4 sFv; M24 sFv; single chain antibody; murine CTLA4; membrane-associated protein, chimeric construct; extracellular domain; human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7; recipient CD28; r-cell proliferation;
Adk18895
Adk18826
Add22194
Adp47098
Adp47098
Adp47098
Adp47098
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Adp47098
Adk18894
Adk18894
Adk18895
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/note= "Corresponds to atc codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
                                      ADP22194
ADP4708B
ADP4709B
ADP4709B
ADP4709B
ADP47024
ADP67224
AM67221
AM676211
AM6762211
AM6762211
AM6762211
AM676221
A
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ80328
ADR46847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xenograft-specific immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY15128 standard; protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-GB001350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-00009280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-murine CTLA-4 M24 sFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2000 (first entry)
 Dorling A;
 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9957266-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lechler IR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
Synthetic.
AAY15128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
AAY15128
 Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp
-G=/Gqn2_1/USFPO spool_p/NoLANDB728463-2/runat_04082005_123943_22574/app_query.fasta_1.5
-G=/Gqn2_1/USFPO spool_p/NoLANDB728463-2/runat_04082005_123943_22574/app_query.fasta_1.5
-DB=A_GG=seeq_OFMT=fastan -SUFPIX=xag -MINMATCH=0.1 -LOOPCL=0_-LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=pct -NONM=ext - HarbasInz=500 -MINNERN=0 -MAXTEN=2000000000
-USER=NOLANO8728463-2 @CGN 1_1 308 @cunat_04082005_123943_22574 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aay15128 Anti-muri
Aab70844 SNV-env 1
Aam48005 Human mon
Adr46821 Human ant
Adr46819 Human ant
Adr46817 Human bet
Adr4687114 Human bet
Adr86877 Human bet
Adr8605 Anti-huma
Adk18605 Anti-huma
                                                                                     ; Search time 90 Seconds
(without alignments)
721.953 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                    1 ATCATCTATCCTGGTGACTC.....GTATTAGCAGCTGGTTAGCC
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                               protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAM48005
ADR46821
ADR46829
ADR46819
ADR46827
ADP47114
ADR18605
ADK18605
                                                                                       2005, 18:21:34
                                                                                                                                                                                                            , Xgapext
, Ygapext
, Fgapext
, Delext
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geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003s:*
geneseqp2003ss:*
geneseqp2003bs:*
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length: 2000000000
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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                                                                                       Run on:
                                                                                                                                           Title:
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Cell-targeting vector selective for T lymphocytes, useful in gene therapy of e.g. acquired immune deficiency syndrome, encodes a single-chain
                                                                                                                                                                                        (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
                                    1. .45
/label= SNV-env_leader
                     Location/Qualifiers
                                                        46. .302
/label= 6C3-scFv
                                                                                                                                                                                                                 Engelstaedter M;
                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 5; 18pp; German.
                                                                                                                                                                  99DE-01046142.
                                                                                                                                          99DE-01046142
                                                                                                                                                                                                                                                                                       of e.g. acquired immune defivariable antibody fragment.
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19.38%
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70.88%
                                                                                                                                                                                                                                         WPI; 2001-246140/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                   N-PSDB; AAF61513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 302 AA;
                                                                                            DE19946142-A1
                                                                                                                                           27-SEP-1999;
                                                                                                                                                                  27-SEP-1999;
                                                                                                                                                                                                                 Cichutek K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                    29-MAR-2001
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Chimeric
                                  Protein
                                                          Protein
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DB:
                       Key
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                                                                                        The present sequence is the anti-murine CTLA-4 sFv (M24 sFv). This is a membrane-associated protein which binds to CTLA-4. Chimeric constructs comprising DNA sequences encoding the extracellular domain of murine CTLA4 and human CDB were used for the study of anti-CTLA4 sFv protein. The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated T-cells and antagoniess the co-stimulatory signal provided by the interaction between donor B7 and recipient CD28. Cells expressing the anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in xenograft-specific immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 AspThrAlaValTyrTyrCysAlaArgPheSerLeuGlyGlyPheAspTyrTrpGlyGln 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 GlyThrLeuValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGly 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 SerAlaLeuAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerValGlyAsp 149
                                                                                                                                                                                                                                                                                                                                                                          50 IleIleTyrFroGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                  70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T lymphocyte, antibody, single chain variable antibody; scFv; human; cell-targeting vector; antivital; cytostatic; immunostimulant; AIDS; gene therapy; immunization; diagnosis, T cell-associated disease; SCID; acquired immune deficiency syndrome; severe combined immune deficiency; T cell lymphoma; fusion construct.
                                                                                                                                                                                                                                                                                                                                                            1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting T-cell mediated rejection of xenotransplanted organs
                                                                                                                                                                                                                                                    240
11
189
                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNV-env leader/human 6C3-scFv fusion construct.
                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                     NOLAN463-2A.SEQ (1-84) x AAY15128 (1-240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB70844 standard; protein; 302 AA
                                                                    Claim 9; Fig 11; 43pp; English.
                                                                                                                                                                                                                                                    0.000165
                                                                                                                                                                                                                                                              114.10
23.08%
22.22%
77.09%
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spleen necrosis virus.
         2000-038815/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 -----
                                                                                                                                                                                                                                                                                       Best Local Similarity:
                      N-PSDB; AAZ29000
                                                                                                                                                                                                                 Sequence 240 AA;
                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                         Alignment Scores:
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25-JUN-2001
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AAB70844
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This invention describes a novel cell-targeting vector (A) containing a DNA sequence (I) encoding a single-chain variable antibody fragment (scFv). The products of the invention have antivoral, cycostatic and immunostimulant activity and can be used in gene therapy, immunization and diagnosis particularly of T cell-associated diseases, specifically acquired immune deficiency syndrome (AIDS), severe combined immune deficiency syndrome (AIDS), severe combined immune celiciency syndrome (AIDS), severe combined immune celiciency (SCID) or T cell lymphoma. (A) target T cells, independently of the CD4 receptor, with high selectivity, 4-5 fold selectivity over thuman B cells, and 1000 fold selectivity, 4-5 fold selectivity over cells, and acceptant, fully defined in the specification. It was used to transform (SNV)) cells, and the specification. It was used to transform (SNV)) cells, channa T lymphocyte) cells, and HeLa (human cervical carcinoma) cells. After 48 hours, the cells were stained with X-gal to determine transformation. The viral titer (infectious units/ml) was over 1 million for D17, I million for CB166 but less than 100 for HeLa, showing the high selectivity for human T cells. This sequence represents the SNV-env lesder/human 6C3-serv fusion construct used in the represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 AspThrAlaMetTyrTyrCysAlaArgValSerGlyTyrCysSerSerThrSerCysTyr 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construction of novel cell targeting vectors described in the invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC--
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23
2
3
3
101
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Matches:
Conservative:
Mismatches:
Indels:
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The invention relates to human monoclonal antibodies or their antigen binding portions that specifically bind to dendritic cells and has one or more of the following characteristics: (a) a binding affinity constant to a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability to opsonise a dendritic cell; (c) the ability to internalise after binding to dendritic cells; or (d) the ability to activate dendritic cells. The isolated human monoclonal antibody or its antigen binding portion may also have any of the following characteristics: (a) mediates cytolysis of dendritic cells in the presence of human effector cells; or (b) inhibits growth of dendritic cells. The antibodies or its antigen binding portion, binds to and blocks the human mannose receptor on dendritic cells. The antibodies have immunomodulatory, antiinflammatory, antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianaemic,
                                      157 AspTyrTyrTyrMetAspValTrpGlyArgGlyThrLeuValThrValSerArg 176
                                                                                                              177 GlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThr 196
                                                                                                                                                                                       .97 GlnSerProSerThrLeuSerAlaSerValGlyAspArgValThrMetThrCysArgAla 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human monoclonal antibodies specific for dendritic cells, useful for inhibiting growth or inducing cytolysis of a dendritic cell and treating or preventing a dendritic cell mediated disease, e.g., autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody; B11; antigen binding portion; dendritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mannose receptor; growth; cytolysis; pathogen; virus; bacterium; autoimmune disease; inflammatory disorder; rheumatoid arthritis; multiple sclerosis; diabetes mellitus; immunomodulatory; antiinflammatory; antiinflammatic; neuroprotective; antiatabetic; antianamic; endocrine; dermatological; antithyroid; uropathic; ophthalmological; muscular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human monoclonal antibody B11 variable heavy chain protein.
                                                                                                                                                                                                                                                        217 SerGlnAsnIleAsnIleTrpLeuAla 225
                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                 58 AGTCAGGGTATTAGCAGCTGGTTAGCC
                                                                                                                                                                                                                                                                                                                                                    AAM48005 standard; protein; 116 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2001; 2001WO-US015114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2000; 2000US-0203126P.
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                          51 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDA-) MEDAREX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deo YM, Keler T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-089788,
N-PSDB; ABA05500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200185798-A2
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endocrine, dermatological, antithyroid, uropathic, ophthalmological and muscular activity. The antibodies or their antigen-binding fragments are useful for inhibiting growth of a dendritic cell, inducing cytolysis of a dendritic cell, inducing cytolysis of a dendritic cell, treating or preventing a dendritic cell mediated disease, detecting the presence of a dendritic cell, targeting an antigen to a bacterium to human mannose receptor on dendritic cells. In particular, the antibodies may be used to treat, autoimmune disease, graft versus host disease, immune system or inflammatory disorders (e.g. rheumatoid pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's syndrome and Graves disease. The present sequence is that of the human monoclonal antibody Bil variable heavy chain, useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; antibody; beta chorionic gonadotropin; antibody; cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; colls agonifit; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody Bl1; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 ileileTyrProGlyAspSerAspThr1leTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CGGGCGAGTCAGGGTATTAGCAGCTGG
                                                                                                                                                                                                                                                                                          116
19
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31
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Mismatches:
                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                             Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR46821 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2004; 2004WO-US002725
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                                                                                                                                                                                                                                                                                                            97.90
36.84%
33.33%
66.15%
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                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                          Sequence 116 AA,
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                                                                                                                                                                                                                                                                           Alignment Scores:
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New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing ecytotoxic T cell response in cancers and infectious diseases.

SEQ ID NO 4; 82pp; English

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) inted to beta human choronic gonadorrogin (betafico), where the antibody comprises a heavy and/or light chain variable region derived from a human choronic gonadorrogin (betafico), where the antibody comprises a heavy and/or light chain variable region derived from a human comprise and the page of a mino acid sequences of SEQ ID NO:30 or 32 (ABR46847, or ABR46849), respectively. Also cescribed: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are inved to betahcs; (2) a molecular conjugate comprising a human antibody that binds to human APCs linked to betahcs; (where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ABR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an activate antigen is processed and presented to T cells in a manner which induces or enhances a T cellmediated response against the antigen; (5) immunising a subject comprising dendritic cells and/or an immunostimulatory agent; and proliferation of endoritic cells and/or an immunostimulatory agent; and proliferation of endoritic cells and/or an immunostimulatory agent; and compinating dendritic cells and/or an immunostimulatory agent; and compinating dendritic cells and/or an immunostimulatory agent; and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate either in vivo or exvivo with APCs such that the antigen is internal sed, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate either in vivo or exvivo with APCs such that the antigen is internal sed, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against eliciting a potent antigen specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present

Sequence 116 AA;

116 19 2 5 5 31 Matches: Conservative: Mismatches: Indels: Length: Gaps: 97.90 36.84% 33.33% 66.15% 0.0111 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

NOLAN463-2A.SEQ (1-84) x ADR46821 (1-116)

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50 ileileTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                        70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC------
                                                                                                                                                                                                                                            ||| :::|||::: ||| || || 90 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106
                                                                                                                                                                                                              78
                                                                                                                                                                                                              ----CGGGCGAGTCAGGGTATTAGCAGCTGG
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ADR46829 standard; protein; 411 AA.

ADR46829 ID ADR4 XX RESULT 5

ADR46829;

18-NOV-2004 (first entry)

Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.

molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betahCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; pB11-betahCG molecular conjugate; fusion protein.

sapiens.

Synthetic.

WO2004074432-A2.

02-SEP-2004.

30-JAN-2004; 2004WO-US002725.

31-JAN-2003; 2003US-0443979P.

(MEDA-) MEDAREX INC.

WPI; 2004-635555/61. N-PSDB; ADR46828

Ramakrishna V; Keler T, Endres M, He L, New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

Claim 16; SEQ ID NO 12; 82pp; English

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCS) inhear antibody conformed to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain, where either or both chains are chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human antibody has to human APCs linked to betahCG; (3) a molecular conjugate comprising a human single conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates a described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates are described above with APCs such that the antigen; (5) immunishing a subject comprising administering any of the molecular conjugates described above with APCs such that the antigen; (5) immunishing a subject comprising doministering any of the molecular conjugate either in vivo or expirating forming a conjugate of the antigen and anothor and antigen, or expired to T cells in a manner which induces or enhances a cytotoxic T (6) inducing or enhancing a cytotoxic T cell response against the antigen is internalised, processed and contacting a conjugate either in vivo or exvivo with APCs such that the andigen is internalised, processed and cytostatic, antimicablai, immunosuppressive, anti-HIV, hepatotropic, cytostatic, antimicablai, immune disorders, cancers and infectious a conjugate by cell criminal activities, and can be used as a CRB agonist, and in vaccines. The methods and compositions of the

CC VHS-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46649), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCS linked to betahCG, where the CC (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjust betahCG, comprising or enhancing a real-mediated immune response, adjuvant; (4) inducting or enhancing a real-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCS such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-comprising administering any of the molecular conjugates described above, cc optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against the antigen is internalised, processed and comprising forming a conjugate of the antigen and a monoclonal antibody with APCs such that the antigen is internalised, processed and comparising forming a conjugate of the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and comparising forming a conjugate of the conjugate of the internalised, processed and comparising forming a conjugate of the conjugate of the conjugate of the ansigen and in vaccines against the antigen. The molecular conjugate and such that the antigen is internalised, processed and corporated and antimalarial activities, and can be used as a CDB agonist, and in vaccines. The methods and compacting methods and conjugate of the processed and and internalised. Processed and and intimalarial activities, and in persent the proce eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present useful for inducing a cytotoxic T cell response, and in particular treating autoimmune disorders, cancers and infectious diseases by invention. 

Sequence 468 AA;

468 22 23 31 Conservative: Mismatches: Indels: Length: Matches: Gaps: 97.90 36.84% 33.33% 66.15% 0.0168 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

x ADR46819 (1-468) NOLAN463-2A.SEQ (1-84)

ò	1 1	1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC	51
qq	69	ValThr	88
ģ	51 .		51
QQ	89 1	89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108	108
δ	52 -		
qa	109 7	109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125	
1			

ADR46827 standard; protein; 613 AA

ADR46827; 

18-NOV-2004 (first entry)

Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; antibody; beta chorionic gonadotropin; antibody; cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;

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The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (RPCS) intended to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human comprises a heavy and/or light chain variable region derived from a human comprises of SEQ ID NO:30 or 32 (ADR4644), or ADR4649), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain antibody that binds to human APC's linked to betahCG, where the conjugate comprising a human single conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates comprising orentacting any of the molecular conjugates of searched to realis in a manner which induces or enhances a realized above with APC's such that the antigen is processed and presented to realis in a manner which induces or enhances a realized propagation of dendritic cells and/or an immunostimulatory agent; and comprising administering any of the molecular conjugates described above, with APC's such that the antigen is internalised, processed and (6) inducing or enhancing a cyctocxic T cell response against the antigen is internalised, processed and compising the antigen is internalised, processed and comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APC's, and contracting the conjugate either in vivo or exvivo with APC's such that the antigen is internalised, processed and compensing and contacting the conjugate either in vivo or curcide and antimalarial activities, and condense actions of the present invention artigen specific cytotoxic T lymphocyte response. Including melanoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing ecytotoxic T cell response in cancers and infectious diseases.
CD8 agonist, vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; betahCG-B11 molecular conjugate; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramakrishna V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 10; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2004; 2004WO-US002725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2003; 2003US-0443979P.
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N-PSDB; ADR46826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keler T, Endres M,
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                                                                                                                                                                                                                                                                                                                                  WO2004074432-A2.
                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                               Synthetic
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613 2 2 5 31

Conservative: Mismatches: Indels:

0.0182 97.90 36.84% 33.33% 66.15%

Best Local Similarity:

Query Match:

Percent Similarity:

Score:

Alignment Scores:

Length: Matches:

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The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Albrehmer's disease, atheroselerosis, and restenosis. The present amino acid sequence represents the heavy chain from a monoclonal antibody that is specific for the human phospholipase A2 (PLA2) enzyme.
                                                                                                                            89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108
                                                            69 ileileTyrProGlyAspSerAspThr1leTyrSerProSerPheGinGlyGlnValThr 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                 Human phospholipase A2-specific monoclonal antibody heavy chain #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feng X;
                                                                                                                                                                                                                                                                                                                                                                                              human, monoclonal antibody, phospholipase A2; PLA2;
inflammatory disorder; degenerative disorder;
joint inflammatory reaction; skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
                                                                                                                                                                                              109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125
                                1 ATCATCTATCCTGGTGACTCTGATACCCACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                ------CGGGCGAGTCAGGGTATTAGCAGCTGG
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Matches:
Conservative:
Mismatches:
Indels:
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NOLAN463-2A.SEQ (1-84) x ADR46827 (1-613)
                                                                                                                                                                                                                                                                 ADP47114 standard; protein; 118 AA.
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(LEXI-) LEXICON GENETICS INC.
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67.65%
61.76%
65.00%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 118 AA;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                     54
                                                                    50 IlelleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                         antiinflammatory; immunomodulator; cytostatic; gene therapy
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                                                                                                                                                                                                                                                                             Anti-human PDGF-D antibody heavy chain protein sequence.
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Matches:
Conservative:
Mismatches:
                                                                                                          -----GCGAGTCAGGGTATTAGCAGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang X,
Gaps:
                        NOLAN463-2A.SEQ (1-84) x ADP47114 (1-118)
                                                                                                                                                                                             ADK18605 standard; protein; 129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-2002; 2002US-00041860
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                                                                                                                                                                                                                                                 (first entry)
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Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-587119/55.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                               WO2003057857-A2
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2003
                                                                                                                                                                                                                         ADK18605;
                                                                                                                                                                 RESULT 9
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1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60 

NOLAN463-2A.SEQ (1-84) x ADK18605 (1-129)

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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGP-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGP-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
78
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-----1leSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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-----lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
                                                                                                                                                                                                                                                                                                                                 antiinflammatory; immunomodulator; cytostatic; gene therapy
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                                                                                                                                                                                                                                                                                    Anti-human PDGF-D antibody protein related sequence #17.
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                                                                                                                                       ADK18791 standard; protein; 129 AA
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                      ADK18791;
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ADK18895
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antiinflammatory; immunomodulator; cytostatic; gene therapy
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Best Local Similarity:
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                                                                                                                                                                                                         Corvalan JRF,
                                       Homo sapiens
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                                                                                              17-JUL-2003
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the cilone 30664188. 0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBF4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                          Weber R;
                                                                                                                                                                                                                                                                                                                                                                            New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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-----IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
                                                                                                           antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                          Gazit G,
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                                                                                 Anti-human PDGF-D antibody protein related sequence #121.
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Matches:
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                                                                                                                                                                                                                                                                                                          Yang X,
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ADK18895 standard; protein; 129 AA
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Best Local Similarity:
                                                                                                                                                                  WO2003057857-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 129 AA;
                                                                                                                                                                                                                                                                                                         Corvalan JRF,
Bezabeh B;
                                                                                                                                        Homo sapiens
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                                                    06-MAY-2004
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                          ADK18895
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DB:
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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antiidiabetic; gene therapy; human; monoclonal antibody; mAb.
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                                                                                                                                                                                      Weber R;
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                                                                                                                                                                                                                                                                                                                                               New human monoclonal antibody that binds to platelet-derived (factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                          Yang X,
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06-JAN-2003; 2003WO-US000398.
                                                           07-JAN-2002; 2002US-00041860
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8 g BXAXEXB

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Homo sapiens.

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an antibody or its binding fragment that binds platelet derived factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                        Larochelle WJ, Lichenstein H;
                                                                                        Keyt B,
                                                                                        Floege J, Gazit-Bornstein G,
                                       16-SEP-2003; 2003WO-US029414.
                                                      16-SEP-2002; 2002US-0411137P
                                                                   (ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.
                                                                                                     WPI; 2004-269881/25.
                                                                                                            N-PSDB; ADL25427
             WO2004024098-A2
                           25-MAR-2004
                                                                                                                                       nephritis.
                                                                                                                         Use of
growth
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Disclosure; SEQ ID NO 38; 115pp; English.

The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of thibiting mesnagial cell proliferation; and (4) a method of training mesnagial cell proliferation; and (4) a method of traininflammatory, dermatological, immunosuppressive and antidabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesnagial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mab) variable region sequence represents a human exemplification of the present invention.

Sequence 129 AA;

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129
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       Length:
Matches:
Conservative:
Mismatches:
                                          Indels:
                                                    Gaps:
                 95.40
57.50%
50.00%
64.46%
         0.0228
                        Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                          Query Match:
        Pred. No.:
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x ADL25428 (1-129) NOLAN463-2A.SEQ (1-84)

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9
             1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT
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                                             61 CAGGGTATTAGCAGC----TGG
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ADP22194

ADP22194 standard; protein; 116 AA (first entry) 09-SEP-2004 ADP22194; 

Human anti-TNFa antibody light chain variable region SEQ ID NO:100

human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antiflammatory; antipsoriatic; antirheumatic; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonis;

induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; rheumatoid arthritis, glomerulonephritis; atherosclerosis; psoriasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis. bladder cancer; lung cancer; glioblastoma; stomach cancer; endometrial cancer; kidney cancer; colon cancer; prostrate cancer; immuno-mediated inflammatory disease; 

Homo sapiens.

WO2004050683-A2

17-JUN-2004

02-DEC-2003; 2003WO-US038281.

02-DEC-2002; 2002US-0430729P.

(ABGE-) ABGENIX INC.

Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S; Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R; Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;

WPI; 2004-480601/45. N-PSDB; ADP22193 New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis.

Example 10; SEQ ID NO 100; 213pp; English.

The present invertion describes a numan monoclonal antibody (1) that the present invertion describes a numan monoclonal antibody (1) that specifically binds to tumour necrois factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 11 amino acid and (b) a light chain CDR1 having the two fully defined 11 amino acid cand (b) a light chain CDR1 having the two fully defined 11 amino acid cand (b) a light chain CDR1 having the two fully described: (1) assaying (CC (M1) the level of TNFa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNFa in the sample; (2) a composition comprising the antibody or its functional fragment and a carrier; (3) treating (M2) an animal suffering from a natural by selecting an animal in need of treatment for the disease by administering the human corlonal antibody of (I); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (I); and animal by selecting an animal in need of treatment for the correction of the sample; (2) antibacterial, antibacterial, antibacterial antibody (I) is useful in the preparation of contribacterial, antibacterial and antiapprosite; antibactoropic, antibacterial, antibactory immunosuppressive, nephrotropic, contribacterial, antibacterial cancer, immunosuppressive, nephrotropic, as a TNFa antagoniat. The antiabody (I) is useful in the preparation of medicament for treating TNF induced apoptosis, neoplastic disease such as thermacoid arthritis, glomerulonephritis, atherosclerosis, psoriassis, restenosis, autoimmune disease, Crohn's disease such as rheumacoid arthritis, glomerulonephritis and antiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the contribation of the present invention. present invention describes a human monoclonal antibody (I) that The

Ŗ Sequence 116

116 19 2 5 31 Matches: Conservative: Mismatches: Indels: Length: 94.90 36.84% 33.33% 64.12% Best Local Similarity: Query Match: Percent Similarity Alignment Scores: Pred. No.:

Gaps:

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                                                      2
                                                                                                                                            70 IleSerAlaAspLysSerIleThrThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                         human, monoclonal antibody, phospholipase A2; PLA2; inflammatory disorder; degenerative disorder; joint inflammatory reaction; skin inflammatory reaction; blood vessels inflammatory reaction; arthritis; psoriasis; asthma; Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feng X;
                                                                                                                                                                                                                                                                                                                                                 Human phospholipase A2-specific monoclonal antibody heavy chain #1.
                                                                                                                                                                                         |||:::
90 AspThrAlaMetTyrTyrCysAlaArgSerGlyTyrGlyMetAspValTrp 106
                                                                                                                                                                        -----CGGGCGAGTCAGGGTATTAGCAGCTGG 78
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Matches:
Conservative:
Mismatches:
Indels:
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Gaps:
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                           NOLAN463-2A.SEQ (1-84) x ADP22194 (1-116)
                                                                                                                                                                                                                                                            ADP47088 standard, protein; 118 AA
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Jia X, Nocerini MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABGE-) ABGENIX INC.
(LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-2003; 2003WO-US038234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-2002; 2002US-0430724P.
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36.21%
32.76%
63.38%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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90 AspThrAlaMetTyrTyrCysAlaArgHisTrpSerTyrGlyMetAspValTrp 107
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NOLAN463-2A.SEQ (1-84) x ADP47088 (1-118)
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Sequence 33, Application US/08665202
| Patent No. 5977322
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Marks, James D. APPLICANT: Schier, Robert | TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to | TITLE OF INVENTION: Tumor Antigens | TITLE OF INVENTION: Tumor Antigens | NUMBER OF SEQUENCES: 141 | CONTRESPONDENCE ADDRESSE: ADDRESSE: Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and T
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTTER: IBM PC compatible
COMPTTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATPONENTY/AGENT INFORMATION:
ANAME: ALCONOME TO THE S-09-490-153-40

US-09-490-153-67

US-09-490-324-67

US-08-490-324-67

US-08-476-3499-81

US-08-65-202-46

US-08-65-202-53

US-08-65-202-54

US-09-315-574-54

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US-09-315-574-54

US-08-65-202-49

US-08-65-202-49

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US-08-65-202-55

US-08-65-202-57

US-08-65-202-57

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US-08-65-202-57

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US-09-315-574-44

US-09-315-574-45

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REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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   RESULT 1
      Command line parameters:

-MODEL=frame+ n2p.model -DEV=x1p

-MODEL=frame+ n2p.model -DEV=x1p

-G=Cqu2 1/VGFTO spool py/NOLAND8728463-2/runat 04082005 123945 22604/app_query.fasta_1.5

-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LGOPCL=0

-LOOPEXT=0 -UNITS=Eits -CFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LGOPCL=0

-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-USER=NOLANO8728463-2 @CGN 1 1 66 @runat 04082005 123945 22604 -NCPU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LGONGLOG

-NOWAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LGONGLOG

-PEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6

-FGAPEXT=0.1 -YGAPOP=10 -YGAPOP=10 -YGAPOP=6
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563.642 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-315-574-33
US-09-726-219A-171
US-08-545-809A-133
US-09-490-025-769B-26
US-09-490-153-26
US-09-490-153-26
US-09-025-769B-40
US-09-025-769B-67
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US-09-025-769B-67
US-09-490-070A-40
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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length: 2000000000
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Perfect score:
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APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tunor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Pour Embarcadero Center, Suite 1100
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ZIP: 94111-4106

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DAY
COMPUTER: DAY
COMPUTER: PATENTION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
RIUNG DATE: 13-JUN-1995
RILING DATE: 13-JUN-1995
RILING DATE: 13-JUN-1996
ATTONEY AGENT INFORMATION:
                                                                                                                                                                                                                                                   283328
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/09315574 Patent No. 6512097
          TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-33
TELECOMMUNICATION INFORMATION:
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92.20
67.65%
58.82%
62.30%
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STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-315-574-33
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y APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Winter, Timochy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REPERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT APPLICATION NUMBER: US 9015198.6
PRIOR PLING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9012845.3
PRIOR FILING DATE: 1990-10-19
PRIOR PILING DATE: 1990-10-19
PRIOR PILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 902453.6
PRIOR APPLICATION NUMBER: GB 90245.3
PRIOR PILING DATE: 1991-03-0
PRIOR PILING DATE: 1991-03-0
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Matches:
Conservative:
Mismatches:
Indels:
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PEPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOLAN463-2A.SEQ (1-84) x US-09-315-574-33 (1-98)
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Johnson, Kevin
Hoogenboom, Hendricus
Griffiths, Andrew
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Holliger, Kasper
Marks, James
Clackson, Timothy
Chiswell, David
                                                                                                                                                                                                                                                                                                              0.00843
92.20
67.65%
58.82%
62.30%
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-726-219A-171
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50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
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CALF: 10044

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATIOR SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025, 769B

PRIOR APPLICATION DATA:

APPLICATION NUMBER: BP 95 11 3021.0

PRIOR APPLICATION DATA:

APPLICATION NUMBER: BP 95 11 3021.0

PRIOR APPLICATION NUMBER: BP 95 11 3021.0

REGISTRATION NUMBER: 27, 7994

REGISTRATION NUMBER: 27, 7994

REGISTRATION NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
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89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 102
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                               55 -----GCGAGTCAGGGTATTAGCAGC-----TGG
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Matches:
Conservative:
Mismatches:
Indels:
           NOLAN463-2A.SEQ (1-84) x US-08-545-809A-133 (1-117)
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                                                                                                                                                                                                                                                                                            RESULT 5
US-09-205-769B-26
Sequence 26, Application US/09025769B
; Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 119 amino acids
amino acid
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62.30%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)596-909
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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STATE: New York
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 133, Application US/08545809A
Fatent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: BOSCH
STATE: MA
COUNTRY: US
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette City Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Diskette Course: Dis
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TELEX: 2001.54
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           92.20
67.65%
58.82%
62.30%
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; ORGANISM: Homo sapiens
US-09-726-219A-171
                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
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US-08-545-809A-133
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                                                                                Alignment Scores:
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Pred. No.:
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PetentIn Release #1.0, Version #1.30 (BPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
PRICE APPLICATION NUMBER: 18-500
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
REPERENCE/POCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 -----GCGAGTCAGGGTATTAGCAGC------TGG 78
70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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Matches:
Conservative:
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ULE TYPE: protein
SNCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                     Sequence 26, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
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US-08-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
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67.65%
58.82%
62.30%
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STATE: D.C.
COUNTRY: USA
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE SEQUENCE US-09-490-070A-26
                                                             RESULT 6
US-09-490-070A-26
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CORPUTER READABLE FOURY disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAWE: Janes F. Haley, Jr., ESQ.
REGISTATION NUMBER: 27,794
REGISTATION NUMBER: 27,794
TELECOMMUNICATION NUMBER: MORPHO/5
TELECOMMUNICATION NUMBER: MORPHO/5
                                                                                                                                                                                             c/o Fish & Neave
GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                         ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOLAN463-2A.SEQ (1-84) x US-09-490-153-26 (1-119)
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/09490324
; Sequence 26, Application US/09490324
; GENERAL INFORMATION:
; APPLICANT: Pack, Peter
; Ilag, Vic
; Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)596-9090
INFORMATION FOR SEQ 1D NO: 26:
SEQUENCE CHRACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.009
92.20
67.65%
58.82%
62.30%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-09-490-324-26
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: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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67.65%
58.82%
62.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-025-769B-67
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                                                      STATE: Ne
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: 24-Dan-2000
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Halley, Jr., ESG.
RECISTRATION NUMBER: 27,794
RECISTRATION NUMBER: 27,794
RECISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG-
                                                                                        c/o Fish & Neave
              Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE: 373
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                    ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOLAN463-2A.SEQ (1-84) x US-09-490-324-26 (1-119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-025-769B-40; Sequence 40, Application US/09025769B; Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.009
92.20
67.65%
58.82%
62.30%
                                                                                                                                                                   COUNTRY: USA
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DB:
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1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG--
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Norman: US / 09/025, 769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
PAPLICATION NORMER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR $50 000
TELEFAX: (212) 596-900
TELEFAX: (212) 596-900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappi, Achim
APPLICANT: 11ag, Vic
APPLICANT: Go, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 -----GCGAGTCAGGGTATTAGCAGC------TGG 78
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70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
20
8
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Mismatches:
Indels:
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Matches:
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TELECOMMUNICATION INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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US-09-490-070A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-490-070A-40

Sequence 40, Application US/09490070A

Sequence 40, Application US/09490070A

Pacent No. 6658248

Pack Peter

Pack, Peter

Inago Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTIONS: 373

CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1995
FILING DATE: 18-MG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                 : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.20
67.65%
58.82%
62.30%
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                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-025-769B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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APPLICANT Knappik, Achim
APPLICANT Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG---
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 -----GCGAGTCAGGGTATTAGCAGC------TGG 78
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
                                      REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISICS:
LENGTH: 120 amino acida
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOLAN463-2A.SEQ (1-84) x US-09-490-070A-40 (1-120)
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REFERENCE/DOCKET NUMBER: 37629-0005
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    92.20
67.65%
58.82%
62.30%
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STRANDEDNESS: <Unknown>
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/025, 769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: James F. Haley, Jr., Bsq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
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70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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Matches:
Conservative:
Mismatches:
Indels:
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REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION:
                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
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TELEPHONE: (202) 912-2000
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TELEPRA: (212)596-9000
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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                                     INFORMATION FOR SEQ ID NO: 67:
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62.30%
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Best Local Similarity:
Query Match:
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US-09-490-153-40
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50 IlelleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
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COMPUTE: New York
COMPUTE: New York
COMPUTE: New York
COMPUTE: READABLE FORM:
MEDIUM TYPE: PLOPBY disk
COMPUTE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION DATA: US/09/490,153
FILING DATE: 18-788-1998
FILING DATE: 18-788-1998
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT Knappik, Achim
APPLICANT Knappik, Peter
Ilaq, Vic
Ge, Liming
Moroney, Simon
Moroney, Simon
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
TELEFAX: (212)596-9090
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,324
FLING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FLING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FLILNG DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                Sequence 40, Application US/09490324;
Patent No. 6828422;
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
GG, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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Conservative:
Mismatches:
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REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: WORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
EMELERAY. (212)596-9000
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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Publication No. US20030167502A1
Fublication No. US20030167502A1
Fublication No. US20030167502A1
Fublication No. US20030167502A1
Fublication No. US20030167502A1
Fublicant: APPLICANT: Keler, Tibor
FITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
FITLE OF INVENTION: CELLS
FUR REPERBNCE: MX1-166
CURRENT FILING DATE: 2001-05-08
FRIOR PILING DATE: 2001-05-08
FRIOR APPLICATION NUMBER: USSN 60/203,126
FRIOR PILING DATE: 2000-09-07
FRIOR PILING DATE: 2000-09-07
FRIOR FILING DATE: 2000-09-07
FRIOR FILING DATE: 2000-09-07
FRIOR FILING DATE: Windows Version 4.0
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US-10-769-144-12

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US-10-769-144-12

US-10-769-144-12

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US-10-041-860-301

US-10-041-860-316

US-10-032-9888-106

US-10-032-928-108

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SUMMARIES
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                                                                                                                                                                                              148
1 ATCATCTATCCTGGTGACTC......GTATTAGCAGCTGGTTAGCC
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                            protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Database :

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Matches:
Conservative:
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; Publication No. US20040248215A1
; GENERAL INFORMATION:
                                                              Sequence 4, Application US/10769144; Publication No. US20040248215A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.90
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CORGANISM: Homo sapiens
US-10-769-144-4
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90 AgpThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106
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; Sequence 4, Application US/10035637
; Publication No. US2030031667A1
; GENERAL INFORMATION:
; APPLICANT: Boo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: CELLS
; TITLE OF INVENTION: CELLS
; TITLE OF INVENTION: CELLS
; TITLE OF INVENTION: CELLS
; TITLE OF INVENTION: CELLS
; TITLE OF INVENTION: CELLS
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-01-09
; PRIOR PILING DATE: 2000-05-08
; PRIOR PELICATION NUMBER: USSN 60/230,739
; PRIOR PELING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
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                                                                                                                                                                       Indels:
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                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                      Percent Similarity:
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Pred. No.:
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Pred. No.:
                                         ; ORGANISM: HC
US-09-851-614-4
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US-10-035-637-4
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     LENGTH: 116
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70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89 -----CGGGCGAGTCAGGGTATTAGCAGCTGG 78 1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC APPLICANT: Relect. Tibor
APPLICANT: Endres, Michael
APPLICANT: Endres, Michael
APPLICANT: Endres, Michael
APPLICANT: Endres, Michael
APPLICANT: Ramakrishna, Venky
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES;
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES;
TITLE OF INVENTION: THRREFOR
TILE REFERENCE: MXI-301
CURRENT PILING DATE: 2004-01-30
FRIOR APPLICATION NUMBER: 60/443979
FRIOR APPLICATION NUMBER: 60/443979
FRIOR APPLICATION NUMBER: 2003-01-31
NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 4 APPLICANT: Relet, Tibor
APPLICANT: Relet, Tibor
APPLICANT: Endres, Michael
APPLICANT: He, Lizhen
APPLICANT: He, Lizhen
APPLICANT: He, Lizhen
APPLICANT: Ramakrishna, Venky
TITLE OP INVENTION: THEREFOR
TITLE OP INVENTION: THEREFOR
TITLE OP INVENTION: THEREFOR
TITLE OP INVENTION: THEREFOR
CURRENT APPLICATION NUMBER: US/10/769,144
CURRENT APPLICATION NUMBER: 60/443979
FRIOR PILING DATE: 2003-01-31
NUMBER OP SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0

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Publication No. US20040248215A1

GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: Remackrishna.
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MXI-301
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: US/10/769,144
CURRENT FILING DATE: 2004-01-30
PRIOR PILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 468
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"Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
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89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108
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109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125
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Sequence 29, Application US/10726332

Publication No. US20050058649A1

GENERAL INFORMATION:

APPLICANT: Gregory M. Landes

APPLICANT: Mary Haak-Frendscho

APPLICANT: Meina Liang

APPLICANT: Mark R. Nocerini

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2

TITLE OF INVENTION: ANTIBODIES THEREOF

FILE REFERENCE: ABGENIX.072A

CURRENT FILING DATE:

PRIOR APPLICATION NUMBER: U/a

PRIOR ELING DATE:

PRIOR ELING DATE:

MINDED OF THE COLUMBER: N/a
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                  APPLICANT: He, Lizhen
APPLICANT: He, Lizhen
APPLICANT: Ramakrishna, Venky
ITILE OF INVENTION: THEREPOY VACCINE CONJUGATES AND USES
ITILE OF INVENTION: THEREPOY
ITILE OF INVENTION: THEREPOY
CURRENT PEPLICATION WUMBER: US/10/769,144
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: 60/443979
PRIOR PILING DATE: 2003-01-31
PRIOR PILING DATE: 2003-01-31
SOFTWARE FREEEE FREEEE (for Windows Version 4.0
SEQ ID NO 10
LIENGTH: 613
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SOFTWARE: FastSEQ for Windows Version 4.0
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Endres, Michael
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US-10-726-332-29
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US-10-726-332-29
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LENGTH: 118
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Percent Similarity:
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US-10-041-860-250
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Sequence 29, Application US/10041860

Publication No. US20303157109A1

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Fend, Xiao-Chi
APPLICANT: Fend, Xiao-Chi
APPLICANT: Fend, Xiao-Chi
APPLICANT: Peng, Xiao-Dong
APPLICANT: Rober, Riancine
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Sancine
APPLICANT: Weber, Sancine
APPLICANT: Weber, Sancine
APPLICANT: Weber, Sancine
APPLICANT: Weber, Sancine
APPLICANT: Weber, Solary
APPLICANT: Weber, Solary
APPLICANT: ANTIBODIES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION WHOBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
ILENGTH: 129
TYPE: PRT
CORCANISM: homo sapiens
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US-10-041-860-215
is Sequence 215, Application US/10041860
is Publication No. US20030157109A1
is GENERAL INFORMATION:
is APPLICANT: Corvalan, Jose R.F.
is APPLICANT: Feng, Xiao-Chi
is APPLICANT: Yang, Xiao-Dong
is APPLICANT: Gazir, Riao-Dong
is APPLICANT: Gazir, Richard
is APPLICANT: Bezabeh, Binyam
is TITLE OF INVENTION: THEREOF
is TITLE OF INVENTION: THEREOF
is FILE REFERENCE: ABGENIX.051A
                                                                                                                                                   55 -----GCGAGTCAGGGTATTAGCAGC------TGG 78
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Matches:
Conservative:
Mismatches:
Indels:
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                                                  NOLAN463-2A.SEQ (1-84) x US-10-726-332-29 (1-118)
Indels:
Gaps:
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Best Local Similarity:
Query Match:
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DB:
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50 IlelleTyrFroGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69
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70 -----IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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APPLICANT: COLVAIAN, JOSE R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 250
LENGTH: 129
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Matches:
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CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 215
LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 250, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
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; ORGANISM: homo sapiens
US-10-041-860-215
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ORGANISM: homo sapiens
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US-10-727-155-100
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Query Match:
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; Sequence 3.9.3.3.
; Sequence 3.9.4.5.
; Publication No. US20040141869A1
; GENERAL INFORMATION:
   APPLICANT: Floseg, Juergen
; APPLICANT: Gazit, Gadi
APPLICANT: Lakochelle, William
; APPLICANT: Lakochelle, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: WSING ANTI-PDGF-DD ANTIBODIES
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PSSESQ for Windows Version 4.0
; SEQ ID NO 38
; LENTH: 129
                                                                                                                                          APPLICANT: Chen, Francines APPLICANT: Chen, Francines APPLICANT: Gazit, Gadi APPLICANT: Weber, Richard APPLICANT: Bezabch, Binyam TITLE OF INVENTION: THEREOF FILE REPERENCE: ANTHONIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF FILE REPERENCE: AGGENIX. 051A CURRENT APPLICATION UNMER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOTTAMRE: FastSEQ for Mindows Version 4.0
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            Application US/10041860
5. US20030157109A1
                            Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Peng, Xiao
APPLICANT: Yang, Xiao-Dong
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ORGANISM: homo sapiens
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US-10-665-383-38
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Query Match:
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Best Local Similarity:
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US-10-665-383-38
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50 ilelleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
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70 -----lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: PACTOR AND USES THEREOF
FILE REFERENCE: AGGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR APPLICATION NUMBER: 60/430729
PRIOR APPLICATION NUMBER: 60/430729
  16
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Matches:
Conservative:
Mismatches:
Indels:
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                                                          NOLAN463-2A.SEQ (1-84) x US-10-665-383-38 (1-129)
Indels:
Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 100
                                                                                                                                                                                                                                                                                                   Sequence 100, Application US/10727155
Publication No. US20050049402A1
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Palaniswami Rathanaswami
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US-10-726-332-3
; Sequence 3, Application US/10726332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rozanne Lee
Kathy Manchulencho
Raffaella Faggioni
Giorgio Senaldi
                                                                                                                                                                             61 CAGGGTATTAGCAGC----
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Scott Klakamp
  64.46%
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Meina Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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Search completed: August 4, 2005, 19:30:17 Job time: 80.75 secs
                 US-10-726-332-5
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Sequence 5, Application US/10726332

Sublication No. US2050058649A1

GENERAL INFORMATION:
APPLICANT: Gregory M. Landes
APPLICANT: Ling Chen
APPLICANT: Yen-Wah R. Lee
APPLICANT: Xiao Feng
APPLICANT: Xiao Feng
APPLICANT: Xiao Chi Jia
APPLICANT: Aiao-Chi Jia
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: Gregory M. Landes
APPLICANT: Gregory M. Landes
APPLICANT: Gregory M. Landes
APPLICANT: Ling Chen
APPLICANT: Wein-wah R. Lee
APPLICANT: Xiao Feng
APPLICANT: Xiao Feng
APPLICANT: Xiao Chi Jian
APPLICANT: Xiao Chi Jian
APPLICANT: Xiao Chi Jian
APPLICANT: Xiao Chi Jia
APPLICANT: Alao Chi Jian
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Mismatches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 118
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93.80
36.218
32.768
63.388
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-726-332-5
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70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
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           Length:
Matches:
Conservative:
Mismatches:
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                                                                               Gaps:
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45.10%
41.18%
63.18%
                                       Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
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Run on:

Sequence:

Minimum DB Maximum DB

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Ig heavy chain V region (clone PBL12) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1281

R;Cai, J; Humphries, C; Richardson, A.; Tucker, P.W.
J; Exp. Med. 176, 1073-1081, 1992

A;Title: Extensive and selective mutation of a rearranged VH5 gene in human A;Reference number: PH1231; MUID:93018822; PMID:1402653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGln----GlyGlnVa
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A;Residues: 1-102 <CAI>
A;Residues: 1-02 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;19-102/Domain: immunoglobulin homology <IMM>
   102
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                     PH1280
PH1258
PH1264
PH1273
PH1271
PH1276
PH1278
PH1278
PH1428
PH1557
A28846
S19670
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S38492
PH1411
S16685
A49047
PH1559
PH1259
PH1267
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PH1413
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S12580
PH1265
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61 CAGGGTATTAGCA
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Best Local Similarity:
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 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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                5.1.6
Compugen Ltd
                                                                                     protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                            283416 segs, 96216763 residues
              GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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PH1409
PH1414
C36006
PH0877
PH1274
S26907
S12424
PH1266
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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seq length: 200000000
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Database :

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Result

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E response: High incidence of
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1414
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J; Bxp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High in dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG----
                                                                                                                                                                                                                                                    Met
                                                                                                                                                                                                                                                A;Noče: the authors translated the codon TTG for residue 119 as C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: GDB.IGH0; IGHDY1
A,Cross-references: GDB:118731; OMIM:146910
A,Map position: 14q32.33-14q32.33
C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Keywords: heteroterzamer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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70 IleSerAlaAspGluSerIleSerThrAlaTyrLeuGlnTrp 83
                                                                                                                                                                                                                                                                                                                                                           127
20
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19
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                                                                                                                                                           A; Reference number: PH1409; MUID: 93115676; PMID: 8418213
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C36006
Ig heavy chain V region (83p2) - human
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93.20
67.65%
58.82%
62.97%
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35.59%
32.20%
62.64%
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A, Residues: 1-127 <VAN>
A, Experimental source: PBMC
                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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Pred. No.:
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                                                                                                         VH5 gene in human B cell chron
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Ig heavy chain V region (clone CORD7) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1249
R;Cai, J; Humphries, C; Richardson, A; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B ce A;Reference number: PH123; MuID:93018822; PMID:1402653
A;Accession: PH1249
A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI>
A;Residues: I-102 <CAI>
A;Roberfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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C; Date: 03-reb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C; Accession: PH409
R; van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A; Title: Molecular evolution of the human immunoglobulin E response: High ir A; Reference number: PH1409; MUID:93115676; PMID:8418213
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A;Molecule type: mRNA
A;Residues: 1-127 < VANA
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology < IMM>
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Matches:
Conservative:
Mismatches:
Indels:
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64.59%
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72 lThrileLeuAla 76
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Ig heavy chain V region (DP-73) - human (Species: Homo sapiens (man) (DD-73) - human (Cispecies: Homo sapiens (man) (Cispecies: E2-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 (Ciscossion: 826607 (PR) (Marks, J.D.; Llewelyn, M.B.; Winter, G. Marks, J.D.; Llewelyn, M.B.; Winter, G. Marks, J.D.; Llewelyn, M.B.; Winter, G. A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: 826885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (5) - human C;Specias: Homo sapiens (man) C;Cpecias: Homo sapiens (man) C;Cpecias: Homo sapiens (man) C;Cpate: 18-Feb-1994 #Bequence revision 10-Nov-1995 #text_change 03-Aug-1998 C;Accession: S12424; S12425; S12426; S12427; S12429; S12432 R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D. EMBO J. 8, 37412748; J899 A; J899 A; Tucker, P.; Capra, J.D. A;Reference number: S09421; MUID:90059975; PMID:2511001
  A,Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12373; NID:g32965; PIDN:CAA78243.1; PID:g32966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Residues: 1-101 <SAN>
A;Cresis-references: EMBL:X56372
A;Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB;
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Matches:
Conservative:
Mismatches:
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A;Cross-references: EMBL:X56373
A;Accession: S12426
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A;Residues: 1-101 <SA3>
A;Cross-references: EMBL:X56370
A;Accession: S12427
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Best Local Similarity:
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C;Species: Homo sapiens (man)
C;Accession: Ph0877
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0877
A;Molecule type: DNA
A;Residues: 1-98 <ARN>
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology of MNA
F;15-98/Domain: immunoglobulin homology of MNA
F;31-58/Domain: immunoglobulin homology of MNA
F;31-35/Region: complementarity-determining 1
F;50-66/Region: complementarity-determining 2
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C'Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C'Accession: PHI279.
S'Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A/Title: Extensive and selective mutation of a rearranged VH5 gene in human A;Reference number: PHI232; MUID:93018822; PMID:1402653
A/Rocession: PHI274
A;Molecule type: DNA
A;Residues: 1-98 cCAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                         90 AspThrAlaMetTyrTyrCysAlaArgHisAsnSerGlnThrGlyAlaSerLeuTrp 108
                                             70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer
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C;Species: Homo sapiens (man)
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Matches:
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Best Local Similarity:
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Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 3.0-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: PH1279
R; Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J; Exp. Med. 176, 1073-1081, 1992
A; Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron A; Reference number: PH1232; MUID:93018822; PMID:1402653
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PHL277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human A;Reference number: PHL277
A;Reference number: PHL277
A;Accession: PHL277
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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Matches:
Conservative:
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A; Residues: 1-102 < CAI>
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Best Local Similarity:
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A;Status: translation not shown
A;Rolecule type: DNA
A;Residues: 1-101 < 8A4>
A;Cross-references: EMBL:X56368
A;Accession: $12429
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 < 8A5>
A;Cross-references: EMBL:X56369
A;Accession: $12432
A;Cross-references: EMBL:X56369
A;Accession: $12432
A;Cross-references: EMBL:X56371
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology < NMA>
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Search completed: August
Job time : 18.75 secs
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: PH1272
R; Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
R; Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
A; Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron A; Reference number: PH1232; MUID: 93018822; PMID: 1402653
A; Accession: PH1272
A; Accession: PH1273
A; Molecule type: DNA
A; Residues: 1-102 < CAI>
A; Residues: 1-102 < CAI>
A; Residues: 1-102 < CAI>
A; Residues: 1-102 < CAI>
A; Residues: 1-102 < CAI>
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                                       Species: Homo sapiens (man)
Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
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Ig heavy chain V region (clone CORD2) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 30 - Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-j
C; Accession: PH1244
R; Cai, J; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A; Title: Extensive and selective mutation of a rearranged VH5 gene A; Reference number: PH1232; MUID: 93018822; PMID: 1402653
A; Accession: PH1234
A; Molecule type: DNA
A; Residues: 1-102 - CAI>
A; Experimental source: cord blood B cell
C; Superfamental source: cord blood B cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 19-102/ Domain: immunoglobulin homology < IMM>
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4, 2005, 19:02:36

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61.7 40.6 427 2 Q9AYR6 61.3 41.4 110 2 Q9JLB3 61 41.2 117 1 HV06 MOUSE 60.8 41.1 293 2 Q73WB2	60.6 40.9 324 2 Q7V9E2 60.5 39.8 517 2 Q9Y781 60.3 39.7 660 1 YG39_PSESM Q886e0 60 39.5 609 2 Q9ARZI 60 39.5 624 2 Q9FMN8 60 39.5 929 2 Q7FBS7 Q7FBS7	27 59.9 40.5 240 2 Q7PKVO Q7PKVO anopheles g 28 59.9 40.5 882 2 Q7PWO Q7PKVO anopheles g 29 59.9 40.5 882 2 Q7PWO Q7PWO G7PWO G7PWO anopheles g 29 59.9 40.5 930 2 Q7PVYO Q7PVYO G7PWO G7P	59.3 40.1 481 2 Q91WT1 Q91Wt1 59.3 40.1 724 2 Q41384 Q41384 59 39.9 460 2 Q66IF9 Q66if9 58.8 39.7 161 2 Q6UF6 Q66if9 58.7 39.7 596 2 Q74C03 Q65P64 58.7 39.7 77 2 Q6EP64 Q6EP64 58.7 39.7 77 2 Q6EP64 Q6EP64 58.7 39.7 793 2 Q7QXX1	58.4 39.5 477 2 Q89HM1 Q89hm1 ALIGNMENTS	RESULT 1 Q921C4 D921C4 LD Q921C4 AC Q922LC4 AC Q922LC4 DT 01-MAY-1999 (TrEMBLrel: 10, Created) DT 01-MAY-1999 (TrEMBLrel: 10, Last sequence update) DT 01-MCT-2003 (TrEMBLrel: 25, Last annotation update) DR Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment). OS Mus musculus (Mouse). OS Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;		Matis L.A., Evans M.J.; "Humanized porcine VCAM-specific monoclonal antibodies w "Humanized porcine VCAM-specific monoclonal antibodies w IgG2/G4 constant regions block human leukocyte binding t endothelial cells."; Mol. Immunol. 34:441-452(1997). EMBL; U78801; AAD00293.1;		Alignment Scores: 12.1 Length: 118 Pred. No.: 70.30 Matches: 13 Score: 70.30 Conservative: 5 Best Local Similarity: 44.83 Mismatches: 7 Query Match: 2.08 Indels: 7 DB: 2.08
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - protein search, using frame_plus_n2p model Run on: August 4, 2005, 18:23:15 ; Search time 80.75 Seconds (without alignments) 1065.378 Million cell updates/sec	Title: Perfect score: 148 Sequence: 1 ATCATCTGGTGACTCGTATTAGCAGCTGGTTAGCC 84 Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.1 Ygapop 10.0, Ygapext 0.1 Ygapop 6.0, Fgapext 0.1 Delop 6.0, Delext 0.1	1612378 segs, 512079187 hits satisfying chosen length: 0	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters:	Database: UniProt_03:*  1: uniprot_sprot:*  2: uniprot_trembl:*  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.  SUMMARIES  Result  No. Score Match Length DB ID  Description	70.3 47.5 118 2 Q921C4 68.3 46.1 111 2 Q9D9B8 68.3 46.1 474 2 Q8R3H6 67.6 45.7 236 2 Q6GMX8 67.3 45.5 2 Q6GMX8 64.4 42.4 302 2 Q919C3 63.6 43.0 117 1 KVII HUMAN 63.6 43.0 127 1 KVII HUMAN 63.6 43.0 127 1 KVII HUMAN 64.6 43.0 127 1 KVII HUMAN 65.6 64.1 65.1 65.1 65.1 65.1 65.1 65.1 65.1 65	427 2 427 2 436 2 436 2 436 2 436 2 427 2.

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Query Match:
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                           4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG 63
                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Testis; MEDILINE=20499374; PUNded=11042159; DOI=10.1i01/gr.145100; Mediline=20499374; PubMed=11042159; DOI=10.1i01/gr.145100; Milbata Y., Shibata Y., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; prepare full-length cDNA ibraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-GT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:17010111 product:immunoglobulin heavy chain 6 (heavy
chain of IgM), full insert sequence.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; Hijah-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CSTBL/6J; TISSUE-Testis;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunioto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Fujiwake S., Inoue K., Tozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riks integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUB-Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                  111 AA.
                                                                                                                                                                  PRT;
NOLAN463-2A.SEQ (1-84) x Q9Z1C4 (1-118)
                                                                                 64 GGTATTAGCAGCT 76
                                                                                                     ----LeuThrAla 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN FANTOM Consortium;
                                                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM N.A.
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ATTACHENCE FOUND NO. TESTIE—Manmary tumoc;

STRAIDECZECH II. TISSUE—Manmary tumoc;

REAUBDETG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

REAUBDETG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

REA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hatch F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.B., Morley K.C., Hale S., Carrinci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RY, Helton B., Ketteman M.J., Madan A., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryzwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse cDNA sequences.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK007163; BAB24877.1; -. HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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68.30
58.62%
44.83%
46.15%
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Best Local Similarity:
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Name=AU044919;
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RESULT 5
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XX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Alusoner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Alusoner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Alusoner R.P., Jordan H., Moore T., Max S.I., Wang J., Heiseh P.K.,

XX Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh P.K.,

XX Alusoner M.J., Usdin T.B., Toahlow M.F., Casavant T.L., Scheetz T.B.,

XX And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Boask S.A., McGwan P.J., McKernan K.J., Matek J.A., Gunarathe P.H.,

XX Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Richards S., Waddan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XX Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RR Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                    MGG; MGG:2144967; AU044919.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR0003595; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; 3.
SMART; SM00406; IGy; I.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00395; IG_MHC; UNKNOWN_1.
PROSITE; PS00395; IG_MHC; UNKNOWN_1.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                          Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474
114
6
7
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
Indels:
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                                          SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUE-Mammary tumor;
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                                                                                                                                       EMBL; BC025447; AAH25447.1;
HSSP; P01869; 1CL7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 GGTATTAGCAGCT 76
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89 ----LeuThrAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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Pred. No.:
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DB:
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OGGMX8
OGGMX9
AC OGGMG
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MEDLINE-218B4657; PubMed=12477922; DOI=10.1073/pnas.242603899;
NEDLINE-218B4257; PubMed=12477922; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Distchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Distchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Exometein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Parage C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Parage C.,
A Robert S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Habey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Myers R.W., Butterfield Y.S.,
A Rizywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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17 PheProGlySerArgCysAspIleGlnMetThrGlnSerProSerSerValSerAlaSer 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 ValGlyAspArgValThrIleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAla 56
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                    Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073764; ARH73764.1; -.
InterPro; IPR005599; IG.
InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
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18
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OT-2004 (TrEMBLrel. 26, Last annotation update)
MGC60843 protein.
MHS musculus (Mouse).
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Matches:
Conservative:
Mismatches:
Indels:
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Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS0835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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45.00$
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLUAR (POTENTIAL).
By similarity.
By similarity.
By similarity.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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MEDLINE-83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
Bentley D.L., Rabbitts T.H.;
"Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
conversion.";
GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; NAS. GO; GO:0006813; P:potassium ion transport; NAS. GO; GO:0006814; P:sodium ion transport; NAS. InterPro; IPR000402; Na/K_ATPase_beta. PEfam; PF00287; Na K-ATPase_bet; 1. TIGRFAMS; TIGR01107; Na KATPase_bet; 1. PROSITE; PS00390; ATPASE_NA K BETA 1; 1. PROSITE; PS00391; ATPASE_NA K BETA 2; 1. ROSITE; PS00391; ATPASE_NA K BETA 2; 1. TRANSMEMDIANE.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-81098966; PubMed-6779204;
Benlley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721E056F04274D0D CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
115 Kappa chain V. I region HK101 precursor (Fragment).
Homo sapiens (Human).
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CARBOHYD
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Am. J. Physiol. 279:R222-R229(2000).
-!- FUNCTION: This is the non-catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of Na (+) and K(+) ions across the plassma membrane.
-!- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0MR-2004 (TrEMBLrel. 26, Last annotation update)
Sodium/potassium-transporting ATPase beta-233 chain (Sodium/potassium-
dependent ATPase beta-233 subunit).
Name-atnb233;
            Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Expressed mainly in epithelial tissues.
-!- SIMILARITY: Belongs to the Na+/K+ and H+/K+ ATPases beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.
L; AJ239317; CAB85586.1; -.
GO:0005890; C:sodium:potassium-exchanging ATPase complex; NAS.
                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO53409; AAH53409.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS00815; IG_LIKE; 5.
PROSITE; PS002909; IG_MHC; UNKNOWN 3.
SEQUENCE 614 AA; 67746 MW; 839BAP3BBD124F89 CRC64;
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112
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                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                     STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
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Mismatches:
Indels:
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TISSUE-Gill;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOLAN463-2A.SEQ (1-84) x Q7TMT6 (1-614)
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67.30
58.62%
41.38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GGTATTAGCAGCT 76
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                                                                         and mouse cDNA sequences.
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                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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DB:
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80
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                 TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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DB:
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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15 LeuCysPheProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TTCCAAGGCCGGCGAGTCAGGGTATTAGCAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotherical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATCATCTATCCTGGT-----GACTCTGATACCACATACAGCCCGTCC---
                                                                                                                                                                                                                                                                    kappa chain V-I region HK101.
                                                                                                                                                                                                                                                                                    Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                            Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                               12799 MW; D7D0FF3718CEF587 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                           similarity
                                                                                                  EMBL; K01322; AAA58930.1; --
EMBL; K01324; AAA58932.1; --
EMBL; V00558; CAA23824.1; --
FIR; A01881; K1HU11.
HSSP; P01607; IBWW.
GO; GO:0005257; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                      Framework-3.
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Framework-1.
                                                                                                                                                                                                                                                                                                  Framework-2
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                                                                                                                                                                                                          Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal.
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63.60
45.24
40.48
42.97
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                                                                                                                                                                                                                                                                                                                     110
1117
1110
Cell 32:181-189(1983)
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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06P1H7
1D 06P1H7
AC 06P1
DT 05-J
DT 05-J
DD 05-J
DD HyPo
OC BUKA
OC MARM
OX NCB1
RN [1]
RN [1]
RN SEQU
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rausberg R.L., Caeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKwan P.J., McKernan K.J., Malke J.A., Gunarate P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., W. Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Mniting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.J., Salaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Ander M., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Salaka U., Smailus D.E., Schnerch A., Schein J.E., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
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Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
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L Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

R BMBL; BC034141; AAH34141.1; -.
R HSSP; Pol607; 1AR2.
R InterPro; IPR001599; Ig.
R InterPro; IPR001599; Ig.
R InterPro; IPR001599; Ig.
R InterPro; IPR001005; Ig_C1.
R InterPro; IPR001006; Ig_MHC.
R InterPro; IPR001006; Ig_WHC.
R InterPro; IPR001006; Ig_WHC.
R R RMART; SM00409; IG; 2.
SMART; SM00409; IG; 1.
R SMART; SM00409; IGC1; 1.
R RAMRT; SM00409; IGC1; 1.
R PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
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63.60
48.72%
46.15%
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Alignment Scores:
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                                                                                 NON TER
SEQUENCE
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                                                                  DISULFID
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DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region VH558 Al/A4. Framework-1.
                                                                Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-1,
                                                                                                                                                                                                                                                             473 AA; 53210 MW; 6F8197395A1C7F79 CRC64;
                                                                                                                                                                                                                                                                                                                         473
113
4
6
6
115
0
                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN'1988 (Rel. 06, Created)
01-JAN'1988 (Rel. 06, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region VHS58 A1/A4 precursor.
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||
99 ThrGlyIleGlyLysTrpPheSer 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CAGGGTATTAGCAGCTGGTTAGCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M13787, AAA38499.1; -.
PIR, A02029; HVMSA1.
HSSP, P01820; 1G7J.
INCERPRO; IPR007110; Ig-like.
INCERPRO; IPR007110; Ig-v.
Pfam; PP00047; ig; 1.
SWART; SW0406; IGv; 1.
IMMUNGGlobulin V region; Signal.
SIGNAL
I 199
CHAIN 20 117 Ig her
DOWAIN 50 54 Comple
                                                                                                                                               EMBL; AAABO1008980; EAA14419.1; -.
InterPro; IPR005654; AFG1_ATPase.
Pfam; PF03969; AFG1_ATPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOLAN463-2A.SEQ (1-84) x Q7Q1B6 (1-473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                         111
63.50
44.74%
34.21%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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No..
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RAY 141

BEQUENCE FROM N.A.

Caraley M.J., Cowenh N.A.,

Caraley M.J., Cowenh R.S.;

Examing M.J., Cowenh R.S.;

Bolphin K.P., Joseph J.A., Fay M.F., Purvis A., Gowing D.,

R. Crawley M.J., Cowen R.S.;

C. Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

C. Tibulose 1.5-bighhosphate, the primary event in photosynthetic carbon dioxide fixation, as well as the oxidative fragmentation of the pentose substrate in the photorespiration process. Both cactions occur simultaneously and in competition at the same active site (By similarity).

C. CATALYTIC ACTIVITY: D-ribulose 1,5-bigphosphate + CO(2) + H(2)O = ATALYTIC ACTIVITY: D-ribulose 1,5-bigphosphate + CO(2) = 3-bigphospho-D-glycarate + 2-phosphoglycolate.

C. CATALYTIC ACTIVITY: D-ribulose 1,5-bigphosphate + CO(2) = 3-bigphospho-D-glycarate - 2-phosphoglycolate.

C. CATALYTIC ACTIVITY: D-ribulose 1,5-bigphosphate + CO(2) = 3-bigphosphate D-glycarate - 2-phosphoglycolate.

C. CATALYTIC ACTIVITY: D-ribulose 1,5-bigphosphate + CO(2) = 3-bigphosphate D-glycarate - 2-phosphoglycolate.

C. CATALYTIC ACTIVITY: D-ribulose 1,5-bigphosphate + CO(2) = 3-bigphosphate (By similarity).

C. CATALYTIC ACTIVITY: D-ribulose 1,5-bigphosphate carboxylase activity; IEA.

DR GO: GO:0005637; C:ribulose bisphosphate carboxylase activity; IEA.

GO: GO:0016894; F:ribulose-bisphosphate carboxylase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Meliceae; Glyceria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
                               Complementarity-determining-2.
                                                                                                                                                               12971 MW; 8B0BC138856DFC9D CRC64;
                                                                                                                                                                                                                                                                   1117
122
4
6
7
                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 AA
                                                                                                    By similarity.
                                                                                                                                                                                                                                                                   Length:
Matches:
   Framework-2.
                                                                 Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOLAN463-2A.SEQ (1-84) x HV52_MOUSE (1-117)
                                                                                                                                                                                                                                                                   126
62.30
55.17%
41.38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GGTATTAGCAGCT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LeuThrAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
68
85
117
115
115
55
69
86 1
41 1
117 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=254778;
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                       ORFNames=CG10353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=CG10353;
                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG10353-PA.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
              RESULT 13
QBMT62
ID QBMT62
AC QBMT62;
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SEQUENCE FROM N.A.

RA Heidelberg J.F., Seehadri R., Havenan S.A., Hemme C.L., Paulsen I.T.,

RA Heidelberg J.F., Esen J.A., Ward N.L., Methe B.A., Brinkac L.M.,

RA Colonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,

RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,

RA Daugherty S.C., DeBoy R.T., Pouts D.E., Haft D.H., Selengut J.,

RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

RA Peterson J.D., Davidsen T.M., Zahou L., Radune D.,

RA Fedblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;

RT The genome sequence of the anaerobic, sulfate-reducing bacterium

RT Desulfovibrio vulgaris Hildenborrough.";

RT Nat. Biotechnol. 22:554-559(2004).

REBL, AE017286; AAS94340.1;
                                                                                                                                                                          99
                                                                                                                                                                                   61 TyrLysGlyArgCys--TyrHisileGluProVal------ProGlyGluGluGly- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACCCTGACTCGCCCGGCCTTGGAAGGACGGCCTGTATGTGGTATCAGAGTCACCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio.
                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Sigma factors serine-protein kinase.
OrderedLocusNames=DVUM0124,
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                   229C3E9FFCE4420B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0878CD5858774397 CRC64;
                                                                     436
113
25
118
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
0 7
10
0 10
Oxidoreductase; Photorespiration; Photosynthesis.
NON TER 1 1 1 NON TER 436 436 436 48417 MW; 229C3E9FFCE4420B C
                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                         138 AA
                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                  NOLAN463-2A.SEQ (1-84) x Q6TL49 (1-436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOLAN463-2A.SEQ (1-84) x Q72WG5 (1-138)
                                                                                                                                                                                                                      67 ATTAGCAGCTGGTTAGCC 84
                                                                                                                                                                                                                                           77 ----GlnTrpileAla 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AA; 15178 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
62.00
41.38$
41.38$
                                                                              62.20
39.47$
34.21$
42.03$
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||| .
67 eAspAsp 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AGATGAT 1
                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                 Query Match:
DB:
                                                                                                                                                                                                                                                                                                     072WG5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                         Q72WG5
                                                                       ..
No.:
                                                                                                                                                                                                                                                                                                                                                                                    8303)
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                                                                                                                                                                                                                                                                   RESULT 12
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685 GluMetLeuIleProTyrLeuMetArgThrPheLysGluLeuSerTyrArgHisGly--- 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Wan X.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
Celniker S.,
                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hakapoda; Insecta; Pterygota;
Neoptera; Endotterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY118358; AAM488817.1; -.
Flybase; FRR003349; CG10353.
InterPro; IPR007632; DUFS90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               984 AA; 112356 MW; 233EFCAAAD0405E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              984
113
6
112
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                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
984 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1043 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             704 ----TrpTyrLysSerHisGlnAspGln 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 TATGTGGTATCAGAGTCACCAGGATAGA
                                                            Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOLAN463-2A.SEQ (1-84) x Q8MT62 (1-984)
                                                     01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-JUN-2003 (TrEMBLrel. 24,
RE04357p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.80
55.88%
38.24%
40.66%
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF04547; DUF590;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A Dedson K., Doug L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Alali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Melson D.L., Rak Reinert K., Remington K., Sunders R.D., Scheeler F., Shen H., R. Shon K., Nison K., Nusskern D.R., Pacleb J.M., R. Shuke B.C., Sden Främen D.A., Waller B.W., Strong R., Sun E., Spradling A.C., Stannfalderon M., Strong R., Sun E., Mulliams S.M., Woodager, Worley K.C., Wu D., Yang S., Pan G., Zhong W., Zhong X., Zhong W., Zhong X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu X., Zhong W. Strience 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patk S., Peiffer B.D., Richards S., Sodergren B.J., Weinskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; melanogaster euchromatic genome sequence."; Gibbs R.A., Rubin G.M.; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The transposable elements of the Drosophila melanogaster euchromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

Mistage S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annotation of the Drosophila melanogaster euchromatic genome: a
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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MEDLINE=22426070; PubMed=12537573;
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FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

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REDUING-20196006; Pubmed-10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Gocayne B.D., Scherer S.E., il P.W., Hookins M.A., Galle R.F., Gocayne G.C., Scherer S.E., It P.W., Hookins M.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Standon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D., RA Baradon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D., RA Ballew R.M., Baau A., Baxendale J., Bayaktaroglu L., Beaseley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Raburis K.C., Busman D.A., Buller H., Cadieu E., Center A., Chandra I., Reson K., Doug D.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Borkova D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Repelson K., Doug D.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P., Burlis K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Andrews D., Harnande J.R., Harris M., Glasser K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Janish M. Kallen P., Karpen G.H., Kavitz S., Kulp D., Lai Z., Lin X., Levitsky A.A., Howland T.J., Wei M.H., Ibegwam C., Janish M. Kallen B., Kodira C.D., Kargt C., Kanison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J., Murphy D.M., Nelson D.L., Markulov G., Milshian N.V., Neberson D., Markulov G., Milshian N.V., Neberson D.K., Nelson D.K., Shen H., Shine B.C., Siden-Klames R.D., Scheeler F., Shen H., Shine B.C., Siden-Klames R., Solien-Klames R., Solien-Klames R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                744 GluMetLeuileProTyrLeuMetArgThrPheLysGluLeuSerTyrArgHisGly--- 762
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                          OEAGBDC5C219FF35 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                          1043 AA; 118845 MW;
EMBL; AE003487; AAF48110.2; -.
IntAct; Q9YYS8; -.
FlyBase, FBgn0030349; CG10353.
InterPro; IPR007622; DUF590.
Pfam; PF04547; DUF590; 1.
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.W., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun; Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Ye H.F., Zaveri J.S., Zhan M., Zhang G., Zheng L., Zheng K.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu Yerse B.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
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MEDLINE=22426069; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Bettennourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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MEDLINE=22426065; PubMed=12537568;
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SEQUENCE 1059 AA; 120767 MW;
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hepatotropic, Fab; hypervariable region, E2 antigen, antibody.
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ABG91923
ABU56809
ABU56809
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ABC21112
ABC9247
ADF10053
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ID ABG76561 standard, protein; 123
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  WPI; 2002-608502/65.
  WO200260954-A1.
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                                                                                                                                                                                                                                                                                1 CGGGCGAGTCAGGGTATTAG.....ACAGCCCGTCCTTCCAAGGC
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                          protein search, using frame_plus_n2p model
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Listing first 45 summaries
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AAU02582
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
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Result

Database :

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The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) El antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments against HCV El or E2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences AGG76513-ABG76568 represent human monoclonal antibodies against HCV El antigen
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Sequence 123 AA;

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25 ArgAlaSerGlyTyrSerPheSerLeuPheTrpValAlaTrpValArgGlnMetProGly 44
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                                                                                                                                                             ||||||::--GluTrpMetAlallelleTyrProGlyAspSerAspThrThrTyrSer 63
                                                                                                                                                     CAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCACATACAGC
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Human pB11-betahCG molecular conjugate protein SEQ ID NO:12. (first entry) 18-NOV-2004 ADR46829; 

molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betahGG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HTV; hepatotropic; virucide; antimalarial; GB agonific; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HTV; hepatitis; malaria; herpes; antibody B11; pB11-betahGG molecular conjugate; fusion protein.

WO2004074432-A2. sapiens. Synthetic. Ношо

02-SEP-2004

30-JAN-2004; 2004WO-US002725.

31-JAN-2003; 2003US-0443979P

(MEDA-) MEDAREX INC

'n Keler T, Endres M,

Ramakrishna V;

He

WPI; 2004-635555/61. N-PSDB; ADR46828.

New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCE) inved to beta human chorionic gonadoropin (Betahco), where the antibody comprises a heavy and/or light chain variable region derived from a human comprises a heavy and/or light chain variable region derived from a human comprises a heavy and/or light chain variable region derived from a human comprise a heavy and/or light chain variable region derived from a human comprise of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy conjugate comprises the tall amno acid sequence of SEQ ID NO:12 (human antibody that binds to human APCs linked to betahcd, where the conjugate comprises the tall amno acid sequence of SEQ ID NO:12 (human antibody that binds to human APCs linked to betahcd, where the conjugate comprises the tall amno acid sequence of SEQ ID NO:12 (as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, with APCs such that the antigen; (5) immunising a subject comprising doministering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugates either in vivo or exvivo with APCs such that the antigen; and conjugate either in vivo or exvivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate either in vivo cell response against the antigen is independent or cells in a manner which induces or enhances eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, heparlitis, malaria and herpes. The present sequence represents a human pBl1-betahCG molecular conjugate, which is used in the exemplification of the present invention. cytotoxic T cell response in cancers and infectious diseases 411 26 0 2 137 Length: Matches: Conservative: Mismatches: Indels: Claim 16; SEQ ID NO 12; 82pp; English 0.000163 113.30 15.76% 15.76% 76.55% Similarity: Sequence 411 AA; Percent Similarity: Best Local Similari Alignment Scores: Query Match:  $\texttt{H}^{\mathsf{X}}(\mathsf{X}^{\mathsf{X}}) \cup \mathsf{COO}(\mathsf$ 

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NOLAN463-2B.SEQ (1-84) x ADR46829 (1-411)

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43		62
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63	63 ProLyBSerLeulleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer 82	82
33		33
83	83 GlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnProGluAspPhe	102
33		33
103	103 AlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProArgThrPheGlyGlnGlyThrLys 122	122
33		33
123	ValGlulleLysGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerGlu 142	142

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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determine the presence or level of adipocytes in a cell of tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease
                                                                                                                                                          183 GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrIleTyrSer 202
                                  143 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuArgIleSer 162
                                                                                                    163 CysLysGlySerGlyAspSerPheThrThrTyrTrpIleGlyTrpValArgGlnMetPro 182
   33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-adipocyte monoclonal antibody heavy chain, FAT 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 144; 182pp; English.
                                                                                                                                                                                                                                                                                                                  AAU02582 standard; protein; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2000; 2000WO-GB003900.
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                                                                                                                                                                                                             84
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                                                                                                                                                                                                                               70 CCGTCCTTCCAAGGC
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N-PSDB; AAS03482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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Alignment Scores:

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their active domains. The polypectides, polymeterides and antibodies raised against the polypeptides, polymeterides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein mammal and prevention of disorders caused by the aberrant protein care used to activity. The polypetides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides or sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in generating the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein antibodies/elicit an immune response, to determine quantitative protein place is set issue markers, and to isolate receptors or ligands.

Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory, cytostatic, neuroprotective, vulnerary, nootropic, anticonvulsant, antiathritic, cerebroprotective, antifungal, antiviral, antibacterial, antialleratic, dermatological, haemostatic, antiasthmatic, thrombolytic, immunogen, antibody, gene therapy, neurological disorder, Parkinson's disease, inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to polynucleotides encoding novel human proteins or
                                                                                                                                                                              61
                                                                                                                                                                                                  GGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
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Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue regeneration; immune disorder.
                                                                                                                                     NOLAN463-2B.SEQ (1-84) x AAU02582 (1-122)
                                                                                                                                                                                                                                                       62 CATACAGCCCGTCCTTCCAAGGC 84
                                                                                                                                                                                                                                                                             59 rgTyrSerProSerPheGlnGly 66
                                                                                                                                                                                                                                                                                                                                                                      AAU14177 standard; protein; 474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001; 2001WO-US002623
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71.76%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel protein #48.
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                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                              AAU14177;
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                                                                                 Query Match:
      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                        AAU14177
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ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, ansemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fingal infection or from autoimmunity, cancer, allergy, asthma, graftversus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention
                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                             47
                                                                                                                                                                                                                                                                                                                       Improved method for antibody treatment - uses an antibody comprising an Old World monkey variable region and a human constant domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-CD4 antibody; monkey; human; therapy; variable heavy domain; old World monkey; constant domain; eczema; immuno-modulated disease;
                                                                                                                                                                                                                                                               ---GGGTATTAGC-
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23
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Matches:
Conservative:
Mismatches:
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92US-00856281.
92US-00912292.
95US-00379072.
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104.40
47.17%
43.40%
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Best Local Similarity:
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                                                                                                                      Sequence 474 AA;
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                                                                                                                                            Alignment Scores:
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10-JUL-1992;
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29-JUL-1998
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DB:
                                                                                                                                                         No.:
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This sequence is the consensus VH5 domain of an anti-CD4 antibody (Ab). This sequence can be used in the method of the invention for treating a subject, where the treatment comprises administration of an Ab. The method comprises the administration of an antibody which has an Old World monkey (e.g. babcon or macaque) variable region which binds to an antigen (Ag) (or Ag binding portion), and a human constant domain. The method is useful for the treatment of ecseme and immuno-modulated diseases and especially rheumatoid arthritis. The recombinant antibodies used are sufficiently different from native monkey antibodies to allow human antibodies used in therapy in prior art, these antibodies do not induce human anti-antibodies used in therapy in prior art, these antibodies do not induce human anti-antibodies on repeated administration. They also have longer half-lives and do not have a lack of effector function with human cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGluSerLeuLys1leSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PR field.)
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103.40
45.28%
43.40%
69.86%
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, Peretz T;
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Best Local Similarity:
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disulfide }
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Query Match:
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The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dGFv). The peptide, optionally in association with or attached, compled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an accute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region
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disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
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characteristics so as to selectively bind target cell in favor of other
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                                            Claim 13; Page 205; 232pp; English.
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                                                                                                                                                                                                                                                                                                       related peptide of the invention
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Plaksin D, Peretz T;
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                    Sequence 98 AA;
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The invention relates to a peptide or polypeptide comprising an Fy molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single cannot very (serP) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Fv molecule, hypervariable region, single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
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                                               Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
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Matches:
Conservative:
Mismatches:
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                                                                                                                                 Claim 13; Page 204; 232pp; English
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103.40
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                 WPI; 2002-619166/66.
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Best Local Similarity:
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29-DEC-2000; 2000US-00751181

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ABG91922 standard; protein; 98 AA
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ID ABG9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GlyGluSerLeuLyBIleSerCyBLyBGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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                                                                                                                                    Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
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                                                  Levanon A;
                                                  Guy R, Lipschitz O, Szanton E,
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                (BIOT-) BIO-TECHNOLOGY GEN CORP
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                                                  Lazarovits J,
                                                                                                     WPI; 2002-619166/66.
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Best Local Similarity:
Query Match:
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                                               Hagai Y, La
Plaksin D,
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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune can seem to restencist, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to danage by anti-disease, anti-cancer or anti-cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases, inflammatory diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-cells in interactions. This sequence represents a human antibody fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
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                                                                                                                                                                                                                                                                                                               Mar-Haim F
Levanon A
                                                                                                                                                                                                                                                                                                         D, Vogel T, Nimrod A,
Kooperman L, Peretz T,
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Matches:
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Amit B, K
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                                                                                                                                                                                                                                                       (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                              31-DEC-2001; 2001WO-US049442.
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29-DEC-2000; 2000US-0258948P.
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Richter T,
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Query Match:
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WO200253700-A2.
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Szanthon E,
                                                       11-JUL-2002
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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as call rolling, metaetasis and important in physiological phenomena such as call rolling, metaetasis and its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment or its complex comprising at least one antibody or its binding fragment or its complex comprising at least one can thook or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metaetasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases, inflammatory diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases cardiovascular diseases such as myocardial infarction, cretinopathic diseases and other diseases mediated by abnormal platelet currents.
                                                                                                                  Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardiar infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Amit B, Kooperman L, Peretz T, Levanon A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated epitope present on cancer cells and important in physiclogical phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                              Human antibody fragment #106.
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                                      04-DEC-2002 (first entry)
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, Richter T,
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Szanthon E,
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Conservative: Mismatches: Indels: Length: Matches: .00163 103.40 45.28% 43.40% 69.86% Similarity: Percent Similarity: Best Local Similari Alignment Scores: Query Match:

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NOLAN463-2B.SEQ (1-84) x ABG91922 (1-98)

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protein interact of the invention

The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one attibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune complexes, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, cell-matrix, platelet-matrix, platelet-complexed tand/or cell-platelet adhesion or aggregation, for increasing complexed tand/or cell-platelet adhesion or aggregation, for increasing complexed cells to disease cells to decreasing the number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases, inflammatory diseases such as acancer, leukaemia, autoimmune diseases, inflammatory diseases cardiovascular diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-compathic diseases caused by sulphated tyrosine-dependent protein-compating calls. 47 54 Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction. GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34 Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular Mar-Haim H; Levanon A; Nimrod A, Peretz T, 84 Plaksin D, Vogel T, Amit B, Kooperman L, TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC Disclosure; Page 280-281; Opp; English Ź (BIOT-) BIO-TECHNOLOGY GEN CORP. ABG91923 standard; protein; 98 Human antibody fragment #107. 31-DEC-2001; 2001WO-US049442 29-DEC-2000; 2000US-00751181. 29-DEC-2000; 2000US-0258948P. (first entry) , Hagai Y, Richter T, diseases, and cancer. WPI; 2002-674776/72. WO200253700-A2. Lazarovits J, Homo sapiens. 04-DEC-2002 11-JUL-2002. Szanthon E, ABG91923; 15 48 22 RESULT 11 ò ð 임 원 

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WPI; 2003-103348/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant chimeric antibodies comprising human, chimpanzee and Old World monkey portions, useful for treating e.g. cancer, eczema, leukemia, lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male infertility.
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                                                                                                                                15 GlyGluSerLeuLyslleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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                                                                                                                                                                                                                                                                                                                         Human; tumour; cancer; systemic lupus erythematosus; immunoglobulin variable region; immunoglobulin variable region; autoimmune response; rheumacoid arthritis; eczema; lymphoma; immunomodulatory disease; leukaemia; Hashimoto's thyroiditis; autoimmune carditis; Addison's disease; type I-diabetes mellitus; multiple sclerosis; male infertility; autoimmune hemolytic anaemia; inflammatory bowel disease; Sjogren's syndrome; psoriasis.
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92US-00856281.
92US-00912292.
95US-00476237.
98US-00082472.
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                                              Percent Similarity:
Best Local Similarity:
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 Sequence 98 AA;
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immunoglobulin variable region. The first and second old World monkey can be the same or different. The recombinant antibody is useful for treating a human having the antigen described above, e.g. for treating cancer in a human having a tumour antigen, or for treating a human suffering from an autoimmune response (where the antigen is involved in an autoimmune response in the human). In particular, the recombinant antibody is useful for treating rheumatoid arthritis, eczema, or an immunomodulatory disease. The recombinant antibody is also useful for treating tumours, leukaemia, lymphoma, Hashimoto's thyroiditis, autoimmune carditis, anderility, autoimmune hemolytic anaemia, inflammatory bowel disease, sjognen's syndrome, psoriasis, or systemic lupus erythematosus. This is sponyapetide for creation of the recombinant antibody
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The present invention describes a method for identifying and obtaining an inhibitor of a pathological process. The method comprises determining if a compound is capable of modulating the binding of the Rc-epsilon-R1 receptor alpha-chain and an autoantibody against the Rc-epsilon-R1 receptor alpha-chain for identifying and obtaining an inhibitor of a pathological process; (2) use of the identified inhibitor for inhibiting activity of the autoantibody against the Rc-epsilon-R1 receptor alpha-chain, and (3) a compound identified by the method, which binds but does not activate the autoantibody against the Rc-epsilon-R1 receptor alpha-chain. The method is useful for obtaining an inhibitor of a pathological process e.g. imbalance between cell-bound and finibitor of a pathological process e.g. imbalance between cell-bound and free IgE e.g. allergic disease (urticaria, late phase allergic reactions, intrinsic astema, drug intolerance and food intolerance). IgE mediated disease or malignancy. The compound is useful for treating a pathological process, particularly conditional autoimmunity. The present sequence
  modulating the binding of the Fc-epsilon-R1 receptor and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain protein sequence from the present invention
                            autoantibody against its alpha-chain.
                                                                             Claim 20; Page 22; 29pp; English.
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## Sequence 98 AA;

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15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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## ABJ18687 standard; protein; 98 AA RESULT 14 ABJ1868

ABJ18687;

(first entry) 06-MAR-2003 Antibody library related human protein sequence SEQ ID No 16.

Library; recombinant antibody; clustering variable region; in silico; immunogenecity; antibody therapeutic; human.

Homo sapiens.

WO200284277-A1

24-OCT-2002.

17-APR-2002; 2002WO-US012202

17-APR-2001; 2001US-0284407P

(ABMA-) ABMAXIS INC

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The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins,
                                                                                    Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source of antibody candidates for further screening for novel antibodies with high affinity against a wide range of antigens and having no or minimum immunogenecity to human subjects treated with antibody therapeutics. This sequence represents a human peptide region of antibody relating to the novel antibody library construction method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and nucleic acids. The libraries constructed are useful as a
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8 유 RESULT 15

ABO27112 standard; protein; 98 AA

ABO27112;

(first entry) 10-SEP-2003

Human germline heavy chain variable region gene segment #45.

Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type. 

Homo sapiens

US2003039649-A1

27-FEB-2003

NOLAN463-2B.SEQ (1-84) x ABO27112 (1-98)

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Length:
Matches:
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Mismatches:
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0.00163 103.40 45.28% 43.40% 69.86%

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Gaps:

Search completed: August 4, 2005, 18:55:57 Job time: 93 secs Applanting

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Patent No. 5681722
GENERAL INPOWMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 639 Prince St.
CITY: Alexandria
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PCC.COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
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6: /cgn2_6/ptodatcal/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodatcal/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-476-349A-81
US-08-665-202-33
US-09-315-574-33
US-09-545-809A-133
US-09-025-769B-26
US-09-490-153-26
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US-09-025-769B-67
US-09-490-070A-40
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Maximum Match 100% .
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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APPLICANT: Newman, Roland A. APPLICANT: Raab, Ronald W. TITLE OF INVENTYON: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince St. CITY: Alexandria
STATE: VA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---------
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CARRENT APPLICATION DATA:
CARRENT APPLICATION OFFICE OF OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                 NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECHONE: 703-836-6620
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 consensus
       US 07/735,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS: not relevant
not relevant
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103.40
45.28%
43.40%
69.86%
APPLICATION NUMBER: US 07
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyllelleTyrProGl 54
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Sequence 33, Application US/08665202

Sequence 33, Application US/08665202

Sequence 33, Application US/08665202

Sether No. 5977322

APPLICANT: Marks, James D.
APPLICANT: Schiet, Robert

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GGGTATTAGC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
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PRICATION NUMBER: US 07/912,292
PILING DATE: 10-ULL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-ULL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHROMOSOME/SEGMENT: VH5 consensus
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid strangers: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: Homo sapiens POSITION IN GENOME:
                                                                                                                                                                                                                                                                                        TELEFAX: 703-836-202.
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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103.40
45.28%
43.40%
69.86%
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Best Local Similarity:
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DATA:
BER: US 60/000,238
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45.28%
43.40%
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                 PRIOR APPLICATION DATA APPLICATION NUMBER: FILING DATE: 14-JUN
                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
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Query Match:
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US-08-545-809A-133
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                                                                                                                                                                                                                                                                                                                          LENGTH:
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Batent No. 6512097

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATM:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC
     APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
GCLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/ACENT INFORMATION:
NAME: HUNTER: TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELEPOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INPORMATION FOR SEQ ID NO: 33:
CONTINUE OF SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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45.28%
43.40%
69.86%
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ------
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-315-574-33
                                                                                                                                                                                                                                                                                                                                                                                                             US-08-665-202-33
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Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: MATSUGA Fuminiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 .-----AGCTGGTTAGCCATCATC
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26
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Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNCEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INPORMATION:
TELEPRAX: (415) 576-0200
TELEPRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AGCTGGTTAGCCATCATCTATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            117
23
1
3
26
2
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APPLICANT: Rnappik, Achim
APPLICANT: Tiag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckchun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
WINMER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 0.-MAY-1993
ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
TELER: 200154
INFORMATION FOR SEQ ID NO: 133: SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
APLING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-025-769B-26; Sequence 26, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          0.000288
103.40
45.28%
43.40%
69.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGCGAGTCA-----
                                                                                                                                                                                                                                                                                   / MOLECULE TYPE: protein US-08-545-809A-133
                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New York
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Best Local Similarity:
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Pred. No.:
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DB:
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34 eGlyfrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlylleileTyrProGl 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               119
23
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26
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
INFORWATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09490070A, Patent No. 6696248
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Pack, Peter
Ilag, Vic
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COMPUTER READABLE FORM:
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103.40
45.28%
43.40%
69.86%
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MOLECULE TYPE: protein
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Best Local Similarity:
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15 GlyGluSerLeuLyg1leSerCygLygGlySerGlyTyr-SerPheThrSerTyrTrp11 34
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Flueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                    NOLAN463-2B.SEQ (1-84) x US-09-490-153-26 (1-119)
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REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
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Patent No. 6828422
GENERAL INFORMATION:
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                       INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
TYPE: amino acid
                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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45.28%
43.40%
69.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                            3 GCCGAGTCA
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Best Local Similarity:
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US-09-490-324-26
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIF: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION' Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGGTATTAGC---
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26
                                                                                                                                                                                                                                                                                                                                                              Gaps:
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TELECOMMUNICATION INFORMATION
                                                     INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGH: 119 amino acida
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                               0.00029
103.40
45.28%
43.40%
69.86%
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                                     TELEFAX: (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
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                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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Pred. No.:
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US-09-490-153-26
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DB:
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No. .
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LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-7698-40
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                   0.00029
                                                                                                                                                   103.40
45.28%
43.40%
69.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                     Alignment Scores:
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ZUP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DETENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FTLING DATE: 18-FBB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .B: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Lining
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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23
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26
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY, FAGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE DOCKET NUMBER: 27,794
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26
                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                    LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
   TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       0.00029
                                                                                                                                                                                                                       103.40
45.28%
43.40%
69.86%
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                       Alignment Scores:
Pred. No.:
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CITY: Ne
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DB:
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15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Per Floppy disk
COMPUTER: Per Floppy disk
COMPUTER: Per Floppy disk
CURRATI PAPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRICK APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Halley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
WUMBER OP SEQUENCES: 373
CORRESPONDENCE ADDRESS:
120
23
1
3
26
2
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Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                NOLAN463-2B.SEQ (1-84) x US-09-025-769B-40 (1-120)
                                                                                     [ndel8:
                                                                                                           Gaps:
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; Patent No. 6300064
; GENERAL INFORMATION:
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TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 aminot
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15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                              NOLAN463-2B.SEQ (1-84) x US-09-490-070A-40 (1-120)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Pack, Peter
Ilag, Vic
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                                    103.40
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Best Local Similarity:
   Alignment Scores:
Pred. No.:
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15 GlyGluSerLeuLyBIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
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                                                   Length:
Matches:
Conservative:
Mismatches:
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NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REGISTRENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40
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SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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45.28%
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69.86%
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STATE: D.C.
COUNTRY: USA
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                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
JS-09-025-769B-67
                                    Alignment Scores:
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15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: TADAPY COMPATIBLE
COMPUTER: TADAPY COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
                                                                                                                                                                                                                                                              48 IGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
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Matches:
Conservative:
Mismatches:
Indels:
Mismatches:
Indels:
Gaps:
                                                                        NOLAN463-2B.SEQ (1-84) x US-09-490-153-40 (1-120)
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REGISTRATION INDEBR: MORPHO/5
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   US-09-490-153-67; Sequence 67, Application US/09490153; Sequence 7, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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69.86%
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   Best Local Similarity:
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Best Local Similarity:
Query Match:
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                      Query Match:
DB:
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                                                                                                                                                                                                          -----AGCTGGTTAGCCATCATCTATCCTGG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                   ----GGGTATTAGC---
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     Conservative:
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APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                      Mismatches:
Indels:
Gaps:
                                                                                             NOLAN463-2B.SEQ (1-84) x US-09-490-070A-67 (1-120)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
WATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
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Pack, Peter
Ilag, Vic
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Pred. No.:
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Sequence 45, App.
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| Sequence 49, Application US/10466242
| Publication No. US2004020887A1
| GENERAL INFORMATION:
| APPLICANT: Drakenberg, Katarina
| APPLICANT: Person, Mats
| TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
| FILE REPERENCE: 0380-P03248US0
| CURRENT FILING DATE: 2004-01-16
| PRIOR APPLICATION NUMBER: US/10/466,242
| PRIOR APPLICATION NUMBER: PCT/SE02/00044
| PRIOR APPLICATION NUMBER: 2002-01-14
| NUMBER OF SEQ ID NOS: 56
| SOUTHWARE: PatentIn version 3.1
| LENGTH: 123
                                                                                               Sequence 49, App.
Sequence 12, App.
                                                                                                                                          Sequence 284,
Sequence 114,
                                                                                                                                                                                                                                                     Sequence Sequence
                                                      Description
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US-10-125-687-16

US-10-041-860-301

US-10-041-860-312

US-10-041-860-312

US-10-041-860-312

US-10-041-860-312

US-10-041-860-336

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US-10-041-860-336

US-10-041-860-336

US-10-041-860-336

US-10-041-860-317

US-10-032-0378-106

US-10-032-0378-106

US-10-032-9888-106

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US-10-032-9888-106

US-10-032-9888-106

US-10-032-9888-106

US-10-032-9268-106

US-10-032-9268-106

US-10-032-9268-106

US-10-032-9268-106

US-10-032-9268-106

US-10-032-9268-107

US-10-10-107-145

US-10-10-107-145

US-10-10-107-145

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US-10-10-107-145

US-10-10-107-145

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US-10-10-107-115-291

US-10-10-10-107-145

US-10-10-107-115-291

US-10-10-10-107-145

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US-10-10-10-107-145
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ORGANISM: Homo sapiens
                             Query
Match
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                             Result
No.
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-MODBL=frame+ 1.2p model -DEV=xlp
-Q=/cgn2 1/USFTO-gpool_pVOLANO8728463-2/runat 04082005_123947_22665/app_query.fasta_1...
-Q=/cgn2 1/USFTO-gpool_pVOLANO8728463-2/runat 04082005_123947_22665/app_query.fasta_1...
-DE=Published Applications AA -QFWT=fastan -SUFFIX=rapb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=20000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -USER=NOLANO8728463-2 @CGN 1_1_260_@runat_04082005_123947_22665_-NCPU=6
-ICPU=3.NO MAMP -LARGQUERY.-NEG SCORES=6 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
                                                                                                                          4, 2005, 19:01:38; Search time 78.75 Seconds (without alignments) 832.849 Million cell updates/sec
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                                                                                                                                                                                                                                                                CGGGCGAGTCAGGGTATTAG.....ACAGCCCGTCCTTCCAAGGC
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| cgn2_6/ptodata/1/pubpaa/DVI PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/DVI NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/DVI NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/DVI NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/DVI NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                        - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                          1752860 seqs, 390397842 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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seq length: 200000000
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Database :

Total number

Minimum DB Maximum DB

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APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR PRILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-35
PRIOR FILING DATE: 2000-09-15
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                                 103 AlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProArgThrPheGlyGlnGlyThrLys 122
                                                                                                                     123 ValGlulleLysGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlyGlyGlySerGlu 142
                                                                                                                                                                                                                                                                                                                                    143 ValGlnLeuValGlnSerGlyAlaGluValLysDysProGlyGluSerLeuArglleSer 162
                                                                                                                                                                                                                                                                                          163 CysLysGlySerGlyAspSerPheThrTyrTrpIleGlyTrpValArgGlnMetPro 182
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Mismatches:
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GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-291-265-284
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                         CAGGGTATTAGCAGCTGGTTAGCCATCATCTGGTGACTCTGATACCACATACAGC 69
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US-10-769-144-12

Sequence 12, Application US/10769144

Publication No. US20040248215A1

GENERAL INFORMATION:
APPLICANT: Realer, Tibor
APPLICANT: Realer, Michael
APPLICANT: Realer, Michael
APPLICANT: Remarkrishna, Venky
TITLE OF INVENTION: THEREOR
TITLE OF INVENTION: THEREOR
TITLE OF INVENTION: THEREOR
FILE REFERENCE: MXI-301
CURRENT APPLICATION NUMBER: US/10/769,144

CURRENT FILLING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: 60/443979
PRIOR FILLING DATE: 2003-01-31

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 411

TYPE: PRI
ORGANISM: Homo sapiens
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Matches:
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CIHER INFORMATION: Clone 2b:7 VH
US-10-466-242-49
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NAME/KEY: PEPTIDE
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ORGANISM: Homo sapiens
FEATURE:
                                ) NAME/KEY: MOD RES
; LOCATION: (19)
; OTHER INFORMATION:
US-09-850-165-89
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US-10-194-975-45
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US-10-125-687-16
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LENGIH: 98
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Fatent No. US20020150580A1
GENERAL INFORMATION:
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: NEWMAN, ROLAND A.
FILE REFERENCE: 037003-0280614
CURRENT PILING DATE: 1097083-0280614
CURRENT FILING DATE: 2001-05-08
FRICR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-04-17
PRIOR PLING DATE: 1995-04-17
PRIOR PLING DATE: 1995-04-17
PRIOR PLING DATE: 1992-03-28
FRIOR PLING DATE: 1992-03-28
FRIOR PLING DATE: 1992-03-28
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FRIOR FILING DATE: 1992-03-28
FRIOR FILING DATE: 1992-07-25
FRIOR FILING DATE: 1992-07-25
FRIOR FILING DATE: 1991-07-25
FRIOR FILING DATE: 1991-07-25
FRIOR FILING DATE: PALEALIN Ver. 2.1
                                                Sequence 114, Application US/10002631C
Publication No. US20030157486A1
GENERAL INFORMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
PRIOR PPLING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 324
SOPTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (2)...(66)
OTHER INFORMATION: Xaa = any amino acid
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104.20
66.67%
57.58%
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                      US-10-002-631C-114
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LENGTH: 301
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LENGTH: 98
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Matches:
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TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: 105/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                 NOLAN463-2B.SEQ (1-84) x US-09-850-165-89 (1-98)
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Sequence 302, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.; APPLICANT: Feng, Xiao-Chi; APPLICANT: Feng, Xiao-Dong; APPLICANT: Chen, Francine; APPLICANT: Gazit, Gadi; APPLICANT: Weber, Richard
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US-10-041-860-301
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Best Local Similarity:
Query Match:
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                                          APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10041860

Sublication No. US2003015710941

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Via, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGANT.031A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 98
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Sequence 16, Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
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ORGANISM: homo sapiens
                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Query Match:
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US-10-041-860-301
Sequence 301, Application US/10041860
Fublication No. US2030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Gazi, Gadi
APPLICANT: Gazi, Gadi
APPLICANT: Heng, Xiao-Chi
APPLICANT: Arg, Xiao-Chi
APPLICANT: Arg, Xiao-Chi
APPLICANT: Heng, Xiao
APPLICANT: Heng, Xiao
APPLICANT: Henge, Rachard
APPLICANT: Henge, Richard
APPLICANT: Weber, Richard
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US-10-041-860-318
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LENGTH: 98
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15 GlyGluSerLeuLysIleSerCys***GlySerGlyTyr-SerPheThrSerTyrTrpIl 34
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Publication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Tia, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Heber, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGAIX.031A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOUTH NOS: 377
SEQ ID NO 312
LENTH: 98
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 98
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Matches:
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US-10-041-860-302
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ORGANISM: homo sapiens
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US-10-041-860-312
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Best Local Similarity:
Query Match:
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NAME/KEY: VARIANT
LOCATION: 23
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LOCATION: 23
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                                                                                                                                                                                                          34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl
                                                                                                                                                                                                                                                                                                                                                   Sequence 318, Application US/10041860
| Publication No. US20030157109A1
| GENERAL INFORMATION:
| APPLICANT: Corvalan, Jose R.F.
| APPLICANT: Feng, Xiao-Chi
| APPLICANT: Feng, Xiao-Dong
| APPLICANT: Feng, Xiao-Dong
| APPLICANT: Reng, Taiao-Dong
| APPLICANT: Reng, Taiao-Dong
| APPLICANT: Gazit, Gadi
| APPLICANT: Weber, Richard
| APPLICANT: Bezabeh, Binyam
| TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION UNMBER: US/10/041,860
| CURRENT FILING DATE: 2002-01-07
| NUMBER OF SEQ ID NOS: 377
| SOFTMARE: FEBLESQ for Windows Version 4.0
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US-10-041-860-318
Percent Similarity:
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; ORGANISM: homo sapiens
US-10-041-860-336
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US-10-041-860-336
is Sequence 336, Application US/10041860
is Publication No. US2030157109A1
is GENERAL INFORMATION:
is APPLICANT: Corvalan, Jose R.F.
is APPLICANT: Vang, Xiao-Chi
is APPLICANT: Yang, Xiao-Chi
is APPLICANT: Chen, Francine
is APPLICANT: Gazit, Gadi
is APPLICANT: Weber, Richard
is APPLICANT: Weber, Richard
is APPLICANT: Weber, Richard
is APPLICANT: Weber, Richard
is APPLICANT: Herman APPLICANT: Weber, Richard
is APPLICANT: Herman APPLICANT: HEREOF
is TITLE OF INVENTION: THEREOF
is TITLE OF INVENTION: THEREOF
is TITLE OF INVENTION: THEREOF
is CURRENT FILLING DATE: 2002-01-07
is NUMBER OF SEQ ID NOS: 377
is SOFTWARE FastSEQ for Windows Version 4.0
is SEQ ID NO 336
is TYPE: PRT
                                           APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THERBOF
FILE REFREENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 390
LENGTH: 98
TWUDE: PRT
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LOCATION: 68
OTHER INFORMATION: Xaa = Any Amino Acid
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Yang, Xiao-Dong
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 Jia, Xiao-Chi
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ORGANISM: homo sapiens
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NAME/KEY: VARIANT
LOCATION: 68
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; Sequence 367, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao-Chi
; APPLICANT: Feng, Xiao-Chi
; APPLICANT: Feng, Xiao-Dong
; APPLICANT: Gazit, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: NATIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
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Search completed: August 4, 2005, 19:30:18 Job time: 79.75 secs

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Ig heavy chain V region (clone PBL8) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
A;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro.
A;Reference number: PH1232; MUID:93018822; PMID:1402653
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A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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Copyright (c) 1993 - 2005 Compugen Ltd.
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH274
B;Cai, J; Humphries, C; Richardson, A.; Tucker, P.W.
J; Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human A;Reference number: PH1232; MUD:93018822; PMID:1402653
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-98 <CAI >
A;Resperimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
Ig heavy chain V region (clone P1-51) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1409
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High ir dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl
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                                                                                                                         A;Accession: PH1409
A;Molecule type: mRNA
A;Residues: 1-127 <VANA
A;Experimental mource: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro.
A;Reference number: PH1232; MUID:93018822; PMID:1402653
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C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C,Accession: PH1279
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A, Molecule type: DNA
A, Residues: 1-102 <CAI>
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Best Local Similarity:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Peb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C;Accession: S12424; S12425; S12427; S12427; S12429; S12432
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism. A;Reference number: S09421; WUID:90059975; PMID:2511001
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GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 37
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                                                           --- AGCTGGTTAGCCATCATCTATCCTGG
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A/Status: translation not shown
A/Status: 1-01 <SA2>
A/Cross-references: EMBL:X56373
A/Cross-references: EMBL:X56373
A/ACCession: S12426
A/Status: translation not shown
A/Molecule type: DNA
A/Status: translation not shown
A/Molecule type: DNA
A/Status: translation not shown
A/ACCESSION: S12427
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SA3>
A/Cross-references: EMBL:X56368
A/ACCESSION: S1243
A/Status: translation not shown
A/MOlecule type: DNA
A/Residues: 1-101 <SA5>
A/Status: translation not shown
A/MOLECULE translation not shown
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A/MOLECULE translation not shown
A/MOLECULE type: DNA
A/RESIGUES: 1-101 <SA6>
A/Cross-references: EMBL:X56371
C/Superfeamily: immunoglobulin V region; immunoglobulin
C/Superfeamily: immunoglobulin homology < IMM>
P/18-101/Domain: immunoglobulin homology < IMM>
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Indels:
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igneavy chain V region (clone PBL3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1272
C;Accession: PH1272
S;Cai, O.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron A;Reference number: PH1232; MUID:93018822; PMID:1402653
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J: Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282.
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A,Rebáldues: 1-102 <CAL>
A,Experimental source: adult PBL
C,Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Residues: 1-102 <CAI>
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Best Local Similarity:
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Ig heavy chain V region (clone PBL12) - human (fragment)

C;Species Homo sapiens (man)

C;Species Homo sapiens (man)

C;Accession: PH1281

R;Cai, J; Humphries, C; Richardson, A; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1993

A;Title: Extensive and selective mutation of a rearranged VHS gene in human B cell

A;Reference number: PH1232; MUID: 93018822; PMID: 1402653

A;Accession: PH1281

A;Residues: 1-102 cCAI>
A;Residues: 1-102 cCAI>
A;Experimental source: adult PBL

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer: immunoglobulin

F;19-102/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jo-Sep-1993 #text_change 16-Aug-1996
C;Accesion: PH1244
R;Cai, J: Humphries, C: Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B ce A;Reference number: PH1232; MUID: 93018822; PMID: 1402653
A;Accession: PH1244
A;Accession: PH1244
A;Residues: 1-102 <CAI>A;Residues: 1-102 <CAI>A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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A; Accession: PH1244
A; Molecule type: mRNA
A; Residues: 1-102 < CAI>A; Resperimental source: EBV-transformed CD5+ B cell [from adult PBL]
A; Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology < IMM>
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Ig heavy chain V region (clone CD-3) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1259

R;Cai, J.; Humphrises, C.; Richardson, A.; Tucker, P.W.

B;Cai, J.; Humphrises, C.; Richardson, A.; Tucker, P.W.

A;Title: Extensive and selective mutation of a rearranged VH5 gene in human

A;Reference number: PH1232; MUID:93018822; PMID:1402653
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A; Residues: 1-102 <CAL>
A; Residues: 1-102 <CAL>
A; Reperimental source: cord blood B cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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Mismatches:
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C;Species: Homo sapiens (man)
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH1258
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Mad. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VHS gene in human B ce A;Reference number: PH1232; MUID: 93018822; PMID:1402653
A;Accession: PH1258
A;Molecule type: DA
A;Residues: 1-102 <CAI>
A;Residues: 1-102 <CAI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IWM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH126, R;Car, R;Car, D; R;Cai, J; Humphries, C; R;Cai, J; Humphries, C; R;Cai, J; Exp. Med. 176, 1073-1081, 1992
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19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl
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C; Keywords: heterotetramer; immunoglobulin P;19-102/Domain: immunoglobulin homology <IMM>
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2 Q9UL96 2 Q924Q0 2 Q925S3 2 Q921Z9 2 Q8Z1R4 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q6B6V3 2 Q9UL9Z 2 Q91V43 2 Q91WT3 2 Q91WT3 2 Q91WT3		PRT; 118 0, Created) 0, Last sequence 5, Last sequence 5, Last sequence 6, Last sequence 7, Last sequence 8,	MW; 90EEC559D3 Length: Matches Commercial Indels: Gaps:
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GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen Ltd.  OM nucleic - protein search, using frame_plus_n2p model  Run on: August 4, 2005, 18:23:15 , Search time 80.75 Seconds  (without alignments)  1065.378 Million cell updates/sec  Title: NOLAN463-2B.SEQ  Perfect score: 148 Sequence: 1 CGGGCGAGTCAGGGTATTAGACAGCCCGTCCTTCCAAGGC 84 Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.1 Ygapop 10.0 , Ygapext 0.1	, Fgapext 0 , Delext 0 , 512079187 ing chosen p 00000 ch 0% ch 100% st 45 summar	line parameters:  1. Incomparison of the control of control of	5 74.7 50.5 117 1 HV05 MOUSE P01550 mus musculu 73.7 49.8 110 2 09JL63 MOUSE P06327 mus musculu 8 73.7 49.8 110 2 09JL63 P0632 MOUSE P06327 mus musculu 9 73.7 49.8 110 2 09JL63 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0632 P0642 P0632 P0642 P0632 P06

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                                                                                  1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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EMBL, BC025447; AAR364711; -...
HSSP; PD1869; 1CL7.
MGD, MGI:2144967; AAR41919.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR003306; Ig_112-11ke.
InterPro; IPR003306; Ig_MC.
InterPro; IPR003595; Ig_-C1.
InterPro; IPR003595; Ig_WC.
InterPro; IPR003595; Ig_WC.
InterPro; IPR003595; Ig_WC.
InterPro; IPR003595; Ig_WC.
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INTERPRO; IPR003595; Ig_WC.
INTERPRO; IPR003595; Ig_WC.
INTERPRO; IRROWN_1.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Mismatches:
Indels:
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                                                                                                                                                                  61 ACATACAGCCCGTCCTTCCAAGGC 84
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59 SerTyrThrGlnLysPheArgGly 66
NOLAN463-2B.SEQ (1-84) x Q9Z1C4 (1-118)
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52.50%
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Best Local Similarity:
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Pred. No.:

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                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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1 CGGCCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:1700110L11 product:immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/60; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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Baltimore D.;
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MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ralusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Datchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
STRAIN=C57BL/6J; TISSUE=Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukuda X., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Andelmatsu M., Hayashizaki Y.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EWBL/GenBank/DDBJ databases.
BEMBI, AKO07163; BAB24877.1; -.
RISSP; PO1820; 1G7J.
RICEPPO: IPRO07210; Ig-like.
RIREPPO: IPRO07210; Ig-like.
RIREPPO: SMART: SMO0406: IG-Y: II-
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Matches:
Conservative:
Mismatches:
Indels:
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65 AsnTyrAsnGlyLysPheLysGly 72
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PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 111 AA; 11976 MW;
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Best Local Similarity:
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1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCTATCCTGGTGACTCTGATACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- MISCELLANEOUS: This germline gene belongs to a set of closely related genes that could encode V regions of NPb antibodies.

PIR, A02032; HYWS02.
PDB; 10X2, NMR; H=20-117.
InterPro; IPR00110; Ig-like.
InterPro; IPR001596; Ig_v.
Ffam; PF00047; Ig; 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
3D-Structure; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region 102.
Framework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                                                                              EMBL, BC053409, AAM53409.1;
HSSP, P01820, 1G7J
INCEPTO: IPRO07110; Ig-like.
INTERPTO: IPRO03597; Ig-cl.
INTERPTO: IPRO03597; Ig-cl.
INTERPTO: IPRO03506; Ig-MHC.
INTERPTO: IPRO03506; Ig-W.
Fam., PPO7654; C1-set, 4.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG-LIKE; 5.
PROSITE; PS00835; IG-LIKE; 5.
PROSITE; PS00839; IG-MHC; UNKNOWN 3.
SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;
                                                                       SEQUENCE FROM N.A.
STRAIN-CSPBL/6NCr; TISSUB-Hematopoietic Stem Cell;
Straubers H.
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Appary chain V region 102 precursor.
Mus musculus (Mouse)
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78 AsnTyrAsnGlyLysPheLysGly 85
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75.70
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Best Local Similarity:
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Percent Similarity:
Best Local Similarit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region VH558 A1/A4. Framework-1.
   Complementarity-determining-2.
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                                                                                                                         12867 MW; 740A65DD851FCA8C CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pheavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA.
                                                            By similarity
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Gaps:
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AsnTyrAsnGlnLysPheLysGly 85
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PIR; A02029; HVMSA1.
HSSP; P01820; 1G7J.
INTERPRO; IPRO07110; IG-like.
InterPro; IPR003596; Ig-v.
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117 AA;
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                                                                                                                                                                                        1 CGGGCGAGTCCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOI=10.1128/IAI.68.10.5803-5808.2000; Malkiel S., Liao L., Cunningham M.W., Diamond B.; Malkiel S., Liao L., Cunningham M.W., Diamond B.; T.Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                           01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
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                                                                                                                                NOLAN463-2B.SEQ (1-84) x HV52_MOUSE (1-117)
                                                                                                                                                                                                                                         61 ACATACAGCCCGTCCTTCCAAGGC 84
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LysTyrAsnGluLysPheLysGly 85
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TyrTyrAsnGlyLysPheLysGly 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with cardiac myosin.";
Infect. Immun. 68:5803-5808 (2000).
EMBL. AF206023, AAF69321.1;
HSSP, P01751; NNOB.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-v.
SMART; SM00406; IGV; I.
PROSITE; PS50835; IG_LIKE; I.
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MEDLINE=20448942; PubMed=10992488;
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2.72
74.70
56.67%
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56.67%
43.33%
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Best Local Similarity:
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SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             Abser, PP07654; L. Bran; PP07654; L. SMART; SM00406; IGv; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 4. PROSITE; PS00290; IG MHC; UNKNOWN 2. AA; 52105 MW; 97DF68D159463F65 CRC64; A81
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                    roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 AA.
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78 LysTyrAsnGluLysPheLysGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             NOLAN463-2B.SEQ (1-84) x Q91WT1 (1-481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                                                                                                                                  EMBL; BC013490; AAH13490.1; -. HSSP; P01751; 1A6W. Pfam; PF07654; C1-set; 2.
                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                       4.58
73.70
60.00%
43.33%
49.80%
                                                                                                                                                                                                                              and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                      musculus (Mouse).
                Igh-VJ558 protein.
                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                               Score:
Percent Similarity:
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Q6PP95;
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AC 06PP
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DT 05-J
DT 05-J
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MEDINESZECH II. TISSUE-Mammary tumor;

MEDINESZOR II. TISSUE-Mammary tumor;

MEDINESZOR II. TISSUE-Mammary tumor;

MEDINESZOR II. TISSUE-Mammary tumor;

MA Klausher R.D., Collins F.S., Wagner L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

M. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

M. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

M. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

M. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

M. Richards S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

M. Richards S.M. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

M. Miting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

M. Miting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

M. Matting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

M. Matting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

M. Matting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

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M. Matting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

M. Matting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

M. Matting M. M., Matting M., Green E.D., Dickson M.C.,

M. Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Matting M., Mattin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 464 AA; 51096 MW; 5B837464D85A1888 CRC64;
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9 9 9 9 0
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Matches:
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INTERPO, IPRO03599; IG.
INTERPO, IPRO03597; IG_C1.
INTERPO, IPRO03597; IG_C1.
INTERPO, IPRO03597; IG_C1.
INTERPO, IPRO03596; IG_WC.
INTERPO, IPRO03596; IG_WC.
INTERPO, IC. G1.
INTERPO, IGC 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ACATACAGCCCGTCCTTCCAAGGC 84
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|TyrTyrAsnGluLysPheLysGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.12
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                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Nammary tumor;

MEDLINE=233825; PubMed=1247931; DOI=10.1073/pnas.242603899;

AL straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schmenn C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schmenn C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schmenn C.M., Haich F.,

An Expleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Bromstein M.J., Usdin T.B., Tonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rack Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Minting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Mammary tumor;

A Strausberg R.;

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

BNB1; BA6837; BA5837.

BNB2; PO1869; 1CL7.

MGD; MGI:96446; 1gh-4.

GO; GO:00042871; C:immunoglobulin complex, circulating; IDA.

GO; GO:0019733; P:antipacterial humoral response (sensu Verte. . .; IDA.

GO; GO:0019733; P:antibacterial humoral response (sensu Verte. . .; IDA.

GO; GO:001788; P:antibacterial humoral response (sensu Verte. . .; IDA.

GO; GO:001788; P:complement activation, classical pathway; IDA.

GO; GO:0006910; P:phagocytosis, engulation bacteria; IDA.

GO; GO:0006911; P:phagocytosis, engulation of immune response; IDA.

GO; GO:0010128; P:positive regulation of immune response; IDA.

GO; GO:0010128; P:positive regulation of type IIa hypersensitivity; IDA.

MGO; GO:0010198; P:positive regulation of type IIa hypersensit. . .; IDA.

InterPro; IPR00310; IG-1ike.

InterPro; IPR00310; IG-1ike.

InterPro; IPR003596; IG-WHC.

InterPro; IPR003596; IG-WHC.

InterPro; IPR003596; IG-WHC.

InterPro; IPR003596; IG-WHC.

InterPro; IPR003596; IG-WHC.

INTERPRO; IPR003596; IG-WHC.

INTERPRO; IPR003596; IG-WHC.

INTERPRO; IPR003596; IG-WHC.

INTERPRO; IPR003596; IG-WHC.

INTERPRO; IPR003596; IG-WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .; IDA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEOUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463
113
110
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
Indels:
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71.70
56.67$
43.33$
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Pred. No.:
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DB:
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42 GlyArg----GlyLeu---GluTrpMetAlaValValHisProSerAspArgThrT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                          Kojima Bookoot, remarka S., Ono T.;
Kojima M., Koide T., Odani S., Ono T.;
"Amino acid sequence of the variable region of heavy chain in immunoglobulin. (Mct) having unusual papain cleavage sites.";
Mol. Immunol. 23.169-174 (1986).
PIR; A02025; HVHUWO.
HSSP; PO1751; HAGW.
GO; GO: 0003576; C: extracellular; NAS.
GO; GO: 0003576; C: extracellular; NAS.
InterPro; IPR00710; Ig-like.
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12
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7
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DOMAIN 1 98 V segment.
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Mismatches:
Indels:
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21-JJJ-1986 (Rel. 01, Last sequence update)
05-JJJ-2004 (Rel. 44, Last annotation update)
105-JJJ-2004 (Rel. 44, Last annotation update)
Name-Igh-VJ558;
                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-I region Mot.
Homo sapiens (Human)
                                                                                                   125 AA
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By similarity.
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Matches:
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D segment.
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84
                              85
                                                                                                     PRT;
                |||||||
TyrTyrSerGluLysPheLysGly
61 ACATACAGCCCGTCCTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrtyrGlyProArgSerGln 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 CATACAGCCCGTCCTTCCAA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7
68.20
53.12%
37.50%
46.08%
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                                                                                                     STANDARD;
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125
96
125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                     HUMAN
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HV05_MOUSE
                                                                                     HV1F_HUMAN
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1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC

NOLAN463-2B.SEQ (1-84) x Q99LC4 (1-463)

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STRAIN=C57BL/6;
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 STTREAMERA
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGGCCGAGTCCAGGGTATTAGCAGCTGGTTAGCCATCATCTTATCCTGGTGACTCTGATACC
                                                  "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-1- MISCELLANEOUS: This germline gene belongs to a set of closely related genes that could encode V regions of NPb antibodies.
                   MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1; Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
VH186.2-0-7-C mu protein (V304-D-J-C mu protein) (Fragment).
Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                   heavy chain V region 3.
                                                                                                                                                                                                                                                                                                                                                                                                                       427C861C53975EDC CRC64;
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122
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Matches:
Conservative:
Mismatches:
Indels:
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Framework-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ACATACAGCCCGTCCTTCCAA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 HistyrAsnGlnLysPheLys 84
                                                                                                                                                                                                                                                                         PFam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                 PINS. A02031; HYMS3.
HSSP; P01810; 2FBJ.
MGD; MGI:96486; IGh-VJ558.
INTERPRO; IPRO07110; IG-like.
InterPro; IPR003596; IG-v.
                                                                                                                                                                                                                                                                                                                                                                                                                       13016 MW;
                                                                                                                                                                                                          EMBL; J00536; AAA38605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.5
67.70
58.62%
41.38%
45.74%
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54
68
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117
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FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                         Baltimore D.;
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Pred. No.:
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CTISSUB-Primary B-Cells;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RETAUSHORE R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B.B., Bronder T., Max S.I., Wang J., Haieh F.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Bokins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Pecers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ray Riczyminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Hones S.J., Marra M.A.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Hymo sapiens (Human).
Eukaryota; Metazoma; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069912; BAB63928.1; -.
EMBL; AB069914; BAB63930.1; -.
PIR; S26744; S26744.
HSSP; P01751; IA6W.
SWART; SM00466; IGV; 1.
NOW TER 143 143
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073764; AAH73764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
03-Mane=V23-D-1gd1;
Name=V23-D-1-1gd1;
Name=V23-D-1-1gd1;
Num musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6;
Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
"The higher density hapten Ag stimulates strong signal to B (submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069864; BAC54573.1; -.
HSSP; PQ1751; 1A6V.
InterPro; IPR007110; Ig-like.
InterPro; IPR007356; Ig-v.
SWART; SM00406; IGV; 1.
PR051TE; PS50835; IG_LIKE; 1.
136 AA; 14882 MW; 99392B1A31F663AF CRC64;
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4, 2005, 19:01:29
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                                             61 ACATACAGCCCGTCCTTCCAA 81
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Job time: 85.75 secs
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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; mimunosuppressive; immunostimulant; immunosupulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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ABR42859
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ABP96287
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2000US-0240816P.
2001US-0276248P.
2001US-0277379P.
2001US-0293499P.
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16-MAR-2001;
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 ABP45310;
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   -MODELE frame + n2p.model -DEV=x1p
-Q=/Cgn2_1/USPTO spool_p/NOLAN463-3A/runat_04082005_120124_18790/app_query.fasta_1.263
-Q=/Cgn2_1/USPTO spool_p/NOLAN463-3A/runat_04082005_120124_18790/app_query.fasta_1.263
-Q=/Cgn2_1/USPTO spool_p/NOLAN463-3A/runat_04082005_120124_10APCEXT=-0 -LAOPEXT=-0 -LAOPEXT=-0 -LAOPEXT=-0 -LAOPEXT=-0 -LAOPEXT=-0 -LAOPEXT=-0 -LAOPEXT=-0 -LAOPEXT=-0 -LAOPEXT=-1 - FRR MAX=100 -TRR MIN=0 -ALIGN=15 -MODE=LOCAL
-OCTEMPT=pto -NORM=ext -HAAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3A @CCN1 1 2.24 @crunat 404082005_120124_18790 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT - DSPBLCOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
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Abp44982 Human BLy
Adg95809 Single ch
Abp4843 Human BLy
Adg95770 Single ch
Add55770 Single ch
Adw62794 Amino aci
Aay65594 Multiple
Abg91903 Human Bry
Abg91903 Human ant
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Compugen Ltd
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(c) 1993 - 2005
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Total number Minimum DB Maximum DB

Searched

Title: Perfect score:

Sequence:

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(first entry

11-MAR-2004

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Erymphocyte Stimulator (ELyS) polypeptides. ELyS is a member of the tumour necrosis factor (TMP) super family and induces B cell twour necrosis factor (TMP) super family and induces B cell trumour necrosis factor (TMP) super family and induces B cell trumour and differentiation. The antibodies of the invention have cytosteatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, theumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP41390-ABP4122B represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
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                                                                Lymphocyte Stimulating polypeptides, useful for the out of cancers and immune disorders.
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Vaughan T, Hilbert D;
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Choi GH,
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                                                                                   treatment
Barash SC,
                                                                Antibodies against B
diagnosis and treatme
                                WPI; 2002-114799/15
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Query Match:
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the lymphocyte stimulator (Buy8). The Buy8 gane has been mapped to chromosome 13934 and encodes a protein that is a member of the tumour chromosome 13934 and encodes a protein that is a member of the tumour conference superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrvs) derived, preferably, from the variable conformation of sich immune, rat or monkey Buy8. The present thereof, of either human, murine, rat or monkey Buy8. The present invention refers to the use of such antibodies in various methods conformation refers to the use of such antibodies in various methods conformation or inappropriate function of Buy8 or its receptor. As such, these compositions are useful for identifying immune disorders conforming mysethenia gravis and multiple sclerosis, infectious disorders disorders e.g. asthma and rheumatoid arthritis, infectious disorates as AIDS and proliferative disorders including leukaemia, carcinoma and conformant Accordingly, they can be described as exhibiting various cotivities such as antirheumatic, antiallergic and cytostatic. This antiinflammatory, antiasthmatic, antiallergic and cytostatic. This cinvention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format cytostatic from WIPO at ftp.wipo.int/pub/published pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatorid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                                           110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS
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            SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BLyS binding scFv SEQ ID 993.
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2001US-0276248P.
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16-MAR-2001;
21-MAR-2001;
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and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (BLOS)). ABP43990-ABP41228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-505530/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                            Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003055979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                           the antibodied
the invention
                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-2003
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proliferation and differentiation. Specifically, it refers to single chain antibody molecules (screw) derived, preferably, it refers to single chain antibody molecules (screw) derived, preferably, it from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and Lymphoma. Accordingly, they can be described as exhibiting various ctivities such as antirheumatic, antiallergic and cytostatic. This colypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format circlely from WIPO at ftp.wipo.int/published pct_sequences.
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## Sequence 250 AA;

```
250
20
3
3
       Length:
Matches:
Conservative:
Mismatches:
                                          Indels:
         0.00327
                 93.80
80.77%
76.92%
67.00%
                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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# DELETED1 (1-81) x ADG95809 (1-250)

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GAAATCAATGATAGTGGAAGCACCAACTACAACCGGTCTCTCAAGAGTCGGGCG----- 54
                                  72
                           AGTCAGGATATTAGCAGC
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                                       70
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Human BLyS binding scFv SEQ ID 954.
                  ABP44943 standard; protein; 253 AA
                                                                                                 (first entry)
                                                                                                 19-AUG-2002
                                                          ABP44943;
ABP44943
```

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

### Homo sapiens.

WO200202641-A1.

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17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0293499P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                 16-JUN-2000; 2000US-0212210P.
                                                                                                       15-JUN-2001; 2001WO-US019110
                                                                                             10-JAN-2002
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(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumpur necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency supdrame (AIDS)). ABP43990-ABP4728 represent the antibodies and fragments of the antibodies described in the method of Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders. Vaughan T, Hilbert D; Claim 1; Page 1540-1541; 3148pp; English Choi GH, Barash SC, the invention Ruben SM,

### Sequence 253 AA;

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253
20
1
3
2
1
      Length:
Matches:
Conservative:
Mismatches:
Indels:
      0.00328
               93.80
80.77$
76.92$
67.00$
                        Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                        Query Match:
DB:
                 Score:
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# DELETED1 (1-81) x ABP44943 (1-253)

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54
           GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG----
                                       55 AGTCAGGATATTAGCAGC 72
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                    20
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                    a
a
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ADG95770 standard; protein; 253 AA.
70
                   RESULT
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ADG95770;

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antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis, asthma; rheumation arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirtheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                            Single chain antibody that immunospecifically binds BLyS SeqID 954
                                                  11-MAR-2004 (first entry)
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#### WO2003055979-A2. Unidentified

10-JUL-2003

14-NOV-2002; 2002WO-US036496

16-NOV-2001; 2001US-0331469P.

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                                                                                                                                                                                                                                                  This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to Chromosome 1344 and encodes a protein that is a member of the tumour can concess factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFx) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aborrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysathenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and luminama. Accordingly, they can be described as exhibiting various cartivities such as antirheumanic, antiallergic and cytostatic. This attivities such as antirheumatic, antiallergic and cytostatic. This colypeptide sequence is a single chain antibody that binds BLyS of the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format con the printed specification, but was obtained in electronic former.
                                                                                                                                               Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immunoglobulin; Ig; transgenic; non-human mammal;
inactivated endogenous Ig locus; B-cell development;
human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
production; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG-----
                                                                         Vaughan TJ, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253
20
1
3
3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                       Example 1; SEQ ID NO 954; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW62794 standard; peptide; 80 AA
                                                                         Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 AGTCAGGATATTAGCAGC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DELETED1 (1-81) x ADG95770 (1-253)
                                  (HUMA-) HUMAN GENOME SCI INC.
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93.80
80.77$
76.92$
67.00$
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                                                                         Barash SC,
                                                                                                              WPI; 2003-505530/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                         Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW62794;
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DB:
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transgenic Xenomice, created using the method of the invention. The predictation describes a transgenic non-human mammal which has genome predictation describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin [Ig] locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus in modified genome also here, and human N-H genes and an inserted human kappa ight chain Ig locus in germline configuration, the human X-H genes and an inserted human kappa light chain Ig locus in germline configuration, the human kappa light chain Ig locus in germline configuration, the human kappa light chain Ig locus where the number of V-H and V-kappa genes, mere the number of V-H and V-kappa genes inserted are selected to restore normal B-cell development in the mammal. The transgenic animals have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New transgenic non-human mammals - having an inactivated immunoglobulin locus and a near complete human immunoglobulin locus, used for production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multiple sclerosis patient CSF B-cell VH region (clone 4d76)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multiple sclerosis, cerebrospinal fluid, CSF; B-cell, heavy chain variable region, VH gene, somatic hypermutation,
                                                                                                                                                                                                                                                                                                                                                  Mendez M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     061190
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                               Klapholz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 71, 128pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY05694 standard; protein; 97 AA
                                                                                                                                                                                                                                                                                                                                               Jakobovits A, Kucherlapati R,
                                                                                                                                                                                                                                 96US-00759620
                                                                                                                                                                       97WO-US023091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.40
74.07$
70.37$
66.00$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---IleSer 53
                                                                                                                                                                                                                                                                                        (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-333314/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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Homo sapiens.
                                                   WO9824893-A2
                                                                                                                                                                       03-DEC-1997;
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                                                                                                             11-JUN-1998.
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AAY05694
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XX
DT 19-0
DT 19-0
DE Mult
XX
XX
Mult
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development of demyelination in CNS of MS. The invention provides

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from DNA of dominant clone 4d76 of B-cells taken from the creebrospinal from DNA of dominant clone 4d76 of B-cells taken from the creebrospinal fluid (CSF) of a multiple sclerosis (WS) parient. Sequences of VH of CSF B-cells were obtained from 4 MS patients (see AAX5316-19). Differences in nucleotide and predicted amino acid (see AAX05691-94) sequences were compared with the closest known germline VH genes; for 4d76, this was RA. The results provided direct evidence that intrathecal clonally expanded e-cells from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that havd undergone antigen selection. This finding implicates an important pathogenic pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-276985/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX25318
                                                                                         Misc-difference
                                                                                                            Misc-difference
                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9915696-A1
                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qin Y;
                                                                                                                                                                                                                                                                                                                                                         Region
                                                  Region
                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                           Region
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This sequence represents a heavy chain variable region (VH) as predicted Determination of B-cell clonality by amplification or enzymatic B-cell clonality; RA gene; diagnosis; human. Æ. Z. note= "replaces Phe of RA" Ŗ. RA" note= "replaces Asn of RA" Leu of RA" /note= "replaces Arg of RA" Phe of RA" note= "replaces Glu of Gly of note= "replaces Gly of Gly of Ser of οĘ . 0 Location/Qualifiers 1. .30 /label= FR1 note= "encoded by note= "encoded by Disclosure, Fig 9D; 67pp; English, note= "replaces note= "replaces note= "replaces note= "replaces note= "replaces note= "replaces 97CA-02216595. 97CA-02220245. 'label= CDR2 98WO-CA000873 31. .36 /label= CDR1 57. .97 /label= FR3 37. .50 /label= FR2 99. .

The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, compled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia. 68 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60 Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---Levanon A; Human Fv molecule hypervariable region related peptide #87. Szanton E, 97 113 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: Guy R, Lipschitz O, Claim 13; Page 193; 232pp; English. ABG78212 standard; protein; 97 AA. (BIOT-) BIO-TECHNOLOGY GEN CORP. 31-DEC-2001; 2001WO-US049440. 29-DEC-2000; 2000US-00751181 DELETED1 (1-81) x AAY05694 (1-97) 0.00375 92.40 74.07% 70.37% 66.00% 15-NOV-2002 (first entry) Lazarovits J, 69 70 WPI; 2002-619166/66. 61 GATATTAGC ---ileser Percent Similarity: Best Local Similarity: Ä WO200259264-A2. Homo sapiens. Alignment Scores: Sequence 97 01-AUG-2002 Hagai Y, I Plaksin D, ABG78212; -20 69 Query Match: DB: .. 02 cells RESULT 9 8 × 8 8 8 8 8 8 8 8 g 셤 ò ò

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the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, lawkaemia, adenoma, lymbona, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one
                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, antibody, epitope, cancer, tumour, cell rolling, inflammation, metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease, cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                         GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG
                                                                                                                                                                                                                                                                                                                       Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mar-Haim H;
Levanon A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nimrod A,
Peretz T,
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Matches:
Conservative:
Mismatches:
Indels:
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Amit B, Kooperman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 269; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG91903 standard; protein; 97 AA.
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                                                                                                                                                                                                                                                                           (1-81) x ABG78212 (1-97)
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Richter T,
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---IleSer 70
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                                                                                                                                                                                                               Best Local Similarity:
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antibody or its binding fragment having a first hypervariable region. The disease, thromosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, cell-matrix, platelet-matrix, platelet to platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for disquosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovaecular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein.

Protein interactions. This sequence represents a human antibody fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human germline heavy chain variable region gene segment #40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type.
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                   the invention
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                                                                                                                                                                                                                                                                                                 Sequence 97 AA;
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The invention describes a meritod of manifest antibody, and appropriate determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodses. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis for selection, for humanisation. The method is useful for making a humanisation. The method is useful for making a humanised antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is immunogenic form suitable for use in an object species. The method is immunogenic form suitable for use in an object species that retain non-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for context the need for determining critically important and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparison of tramework sequences to represent a human hand human and human antibodies. This sequence transfer the represents a human hand human need for comparison to represent a human hand non-human and human antibodies. This sequence
                         method of making a humanised antibody
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                         The invention describes a
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Sequence 97 AA

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064440
       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                       DELETED1 (1-81) x ABO27107 (1-97)
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70.37%
66.00%
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Alignment Scores:
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            61 GATATTAGC
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ADB75646 standard; protein; 97 AA (first entry) 04-DEC-2003 ADB75646; 

RESULT 12

Human protein relating to the invention SEQ ID NO:55.

antibody library, CD1 region, CD2 region, VH region, VL region, immunoglobulin, CD3 region; TM1 scFv; human.

Homo sapiens.

WO2003044198-A1

30-MAY-2003

22-NOV-2002; 2002WO-JP012236.

22-NOV-2001; 2001JP-00358602

(UYKE-) UNIV KEIO.

Okui Takayanagi A, Shimizu N,

Ξ

WPI; 2003-449818/42.

Highly stable artificial antibody libraries with super-repertory and

Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a CDNA library as template for amplifying a fragment containing the CD1 and CD2 regions of the WH or VL region of immunoglobulin gene and a fragment containing the CD3 region by PCR, respectively, producing WH and VL libraries, transferring into a host, and displaying the single-stranded antibody on a phage surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents a protein of the invention. 1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60 89 B-cell; malignant; immunoglobulin; immunoglobulin variable region; Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; contamination from unexpressible ones, useful as tool in proteomics and e.g. for diagnosis and treating various diseases 0 1 1 1 0 0 Lymphoma related immunoglobulin variable region F5. Conservative: Mismatches: Indels: Length: Matches: Disclosure; Page 101; 108pp; Japanese. ADD28104 standard; protein; 97 AA (CANC-) CANCER RES TECHNOLOGY LTD 07-MAR-2002; 2002GB-00005395 24-FEB-2003; 2003WO-GB000783 (1-81) x ADB75646 (1-97) 0.00375 92.40 74.07**\$** 70.37**\$** 66.00**\$** 15-JAN-2004 (first entry) non-Hodgkin's lymphoma ---IleSer 70 61 GATATTAGC 69 Zhu D, Stevenson F; Best Local Similarity: WO2003074059-A2. Sequence 97 AA; Percent Similarity: Synthetic. Homo sapiens. Alignment Scores: 12-SEP-2003 ADD28104; 69 Query Match: DB: normal .. 9 RESULT 13 DELETED1 셤 HALL STATES AND STATES Š ò

Example 6; Fig 16a; 135pp; English

positions.

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The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (1g) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (l) treating a patient suffering from or at risk of having lymphoma; (2) screening a patient suffering from cor at risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the lgy variable region of the B cell receptor inhibiting glycosylation of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (S) has glycosylation inhibitor. The method is useful in classifying a B-cell as medicament for treating non-Hodgkin's lymphoma. The present sequence medicament for treating non-Hodgkin's lymphoma. The present sequence represents an Ig variable region sequence which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
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              Disclosure; Fig 4; 61pp; English.
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29-MAY-2002; 2002US-0384197P.
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                                                                                                                                                                                                                                                                                             exemplification
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen blinding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATCAATCATGGGAGGGACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF10150 standard; protein; 97 AA
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29-MAY-2002; 2002US-0384197P.
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Example 16; Fig 40a; 135pp; English.
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The present invention relates to a method for optimizing at least one physic-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention. 

Sequence 97 AA;

97 113 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 0.00375 92.40 74.07\$ 70.37\$ 66.00\$ Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: Score:

DELETED1 (1-81) x ADF10150 (1-97)

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61 GATATTAGC 69

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Search completed: August 4, 2005, 19:34:16 Job time : 120 secs

116, Appl 116, Appl 117, Appl 113, Appl 113, Appl 1140, Appl 1140, Appl 1140, Appl 1141, Appl 1142, Appl 1142, Appl 1143, Appl 1143, Appl 1143, Appl 1143, Appl 1143, Appl 1143, Appl 1144,

OM nucleic

Run on:

Sequence:

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APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESSONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6
Sequence 3
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US-09-802-096-5
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US-09-371-276-835
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US-09-371-276-835
US-09-374-165-16
US-09-374-165-14
US-09-374-167-14
US-09-138-091A-45
US-09-138-091A-45
US-08-851-362D-35
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US-08-951-362D-35
US-09-138-091A-142
US-09-490-070A-65
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US-09-490-153-65
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US-09-491-148-79
US-09-138-091A-77
US-09-716-76-850
US-09-716-76-850
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ZIP: 02110-2804

COMPUTER READABLE Diskette

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                                                                                                                                          CITY: E
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       Command line parameters:
-MODEL=frame+ n2p.model -DEV=Xlp
-MODEL=frame+ n2p.model -DEV=Xlp
-Q=/con2_1/USFTO_spool_p/NOLAN463-3A/runat_04082005_120126_18820/app_query.fasta_1.263
-Q=/con2_1/USFTO_spool_p/NOLAN463-3A/runat_04082005_120126_18820/app_query.fasta_1.263
-D=18sued_Patents AA -QFWT=fastan -SUFFTX=xii -MINWATCH=0.1 -LOOPEL=0
-LIST=E45 -DOCALIGN=200 -THE SCORE=PQT -THE MAX=100 -THE MINE_0 -ALIGH=15
-MODE=LOCAL_OUTFMT=pdt -NORM=ext -HEAF912E=500 -MINLEN=0 -NAXLEN=20000000
-USER=NOLAN463-3A_@CGN 1 146 @runat_04082005_120126_18820 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG_SCORES=0 -MAXTT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELDP=6 -DELEXT=0.1
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25, Appli
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Appli
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Sequence E
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11: /cgn2_6/ptodatca/1/iaa/5A_COMB.pep:*
12: /cgn2_6/ptodatca/1/iaa/5B_COMB.pep:*
13: /cgn2_6/ptodatca/1/iaa/6A_COMB.pep:*
14: /cgn2_6/ptodatca/1/iaa/6B_COMB.pep:*
15: /cgn2_6/ptodatca/1/iaa/PCTUG_COMB.pep:*
16: /cgn2_6/ptodatca/1/iaa/PCTUG_COMB.pep:*
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18: /cgn2_6/ptodatca/1/iaa/PcTUG_COMB.pep:*
18: /cgn2_6/ptodatca/1/iaa/backfiles1.pep:*
18: /cgn2_6/ptodatca/1/iaa/backfiles1.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                    - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-545-809A-118
US-08-793-450-4
US-09-203-768A-2
US-08-793-450-8
US-09-372-425A-6
US-09-490-070A-25
US-09-490-153-25
US-09-490-153-25
US-08-45-809A-137
US-08-46-151-5
US-08-46-163B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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987.4
981.4
981.4
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981.4
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Result

Minimum DB Maximum DB

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                             APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KAZCOREK, MICHEL
APPLICANT: CHABHHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: P.C.
1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 533
                                                                                                                                                         116
119
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                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: FR 94/10566
ATTORING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     0.000397
92.40
74.07%
70.37%
66.00%
                SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 123 amino acids
amino acid
INFORMATION FOR SEQ ID NO:
                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-4
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Best Local Similarity:
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ZIP: 22202
                                                                                       ; MOLECULE TYPE:
US-08-545-809A-118
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STATE: VA
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US-08-793-450-4
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DB:
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Sequence 2, Application US/09203768A

Sequence 2, Application US/09203768A

GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Of Use
TITLE OF INVENTION: Of Use
TITLE OF INVENTION: Of Use
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
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APPLICANT: EDELMAN, LENA
APPLICANT: MARCARITYE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
ITITE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
ITITE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
ITITE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
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Length:
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Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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70.37%
66.00%
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74.07%
70.37%
66.00%
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US-09-203-768A-2
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Best Local Similarity:
                                              Percent Similarity:
Best Local Similarity:
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Query Match:
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119
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
                                                                        CURAL...

PILING DATE: 03-PL...

PILING DATE: 03-PL...

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: 08LON, NORMAN P.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-3220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: ATZ amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: alinear
DECORET
                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELETED1 (1-81) x US-08-793-450-8 (1-472)
                                                                                                                                                                                                                                                                                                                                                                                                                   0.000659
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74.07$
70.37$
66.00$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-372-425A-6
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGGGAGTCAG 60
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; Sequence 25, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
APPLICANT: Knapplk, Achim
APPLICANT: Rnapplk, Achim
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Hag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
VUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEBE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
COUNTRY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNICT: USA
ZIP: U021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 10-FEB-1998
FRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY AGENT TRFORMATION:
NAME: James F Haley, Jr., EEG.
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: Heavy chain without Tailpiece - AA
                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                        ATTORNEY/AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECOMMUNICATION INFORMATION:
TELEFAX: (310) 788-5000
TELEFAX: (310) 788-5100
TELEFAX: (310) 788-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                      0.00305
                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.07$
66.67$
62.43$
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: LUCH
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PELOS/MS-DOS
SOFTWATING SYSTEM: PC-DOS/MS-DOS
SOFTWATING SYSTEM: PC-DOS/MS-DOS
SOFTWATION NUMBER: US/09/490.070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
RECISTRATION NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
Plueckthun, Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Esg. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                118
118
12
6
6
                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/09490070A
Patent No. 66548
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
TELEPHONE: (212)596-9000
TELEPAX: (212)596-90900
INPORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid STRANDEDNESS:
TOPOLOGY: linear
NOLECULE TYPE: protein
US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
STATE: D.C.
COUNTRY: USA
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70.37$
66.67$
60.29$
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-490-070A-25
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No
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50 GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
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COMPUTER READABLE FORM:

MEDUUM TYPE: Floppy disk

CONFUTER: IBM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 14-Jan-2000

PRIOR APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAWE: James F. Haley, Jr., EEG.

REGISTRATION NUMBER: MORPHO/5

TELECOMMUNICATION NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

NAME: James F. Haley, Jr., F. EEG.

REGISTRATION NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSER: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                              Indels:
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                      Gaps:
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;
TOPOLOGY: linear
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                        84.40
70.37%
66.67%
60.29%
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                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-08-545-809A-137
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STATE: MA
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 Query Match:
DB:
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                                                                                                                                                                 1 GARATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                     50 GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

WEDUW TYPE: Floppy disk

WEDUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

COBERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 12-Jan-2000

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                               Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
                118
18
2
6
6
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18
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               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLGGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                  Gaps:
                                                                                                                                 DELETED1 (1-81) x US-09-490-153-25 (1-118)
                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/09490324
Patent No. 6826422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                 84.40
70.37$
66.67$
60.29$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.40
70.37%
66.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0049
                0.0049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                61 GATATTAGC 69
                                                                                                                                                                                                                                                              69 ---ileSer 70
                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
ignment Scores:
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Pred. No.:
                                                                                                                                                                                                                                                                                                RESULT 9
US-09-490-324-25
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
115
0
0
   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRION APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/POCKET NUMBER: 06501/004001
TELEPHONE: 617-542-8006
TELEPHONE: 617-542-8006
TELEPHONE: 617-542-8006
TELERS: 200154
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELETED1 (1-81) x US-08-545-809A-137 (1-120)
                                                        DELETED1 (1-81) x US-09-490-324-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                            Sequence 137, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 amino acids
60.29%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.00
79.17
62.50
57.86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GATATTAGCAGC 72
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                                                                                                                                                                                                   69 ---IleSer 70
                                                                                                                                                                    61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boston
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Percent Similarity:
Best Local Similarity:
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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70 --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                   Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::|||
ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 CAGGATATTAGC--------
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18
2
2
2
2
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA: APPLICATION DATA: US/08/466,151
CLASSIFICATION NUMBER: US/08/466,151
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/466163
FILING DATE: 15-MAR-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1992
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/879495
FILING DATE: 14-AUG-1991
ATTORNEY APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/8794768
FILING DATE: 14-AUG-1991
ATTORNEY APPLICATION NUMBER: 07/8794768
FILING DATE: 14-AUG-1991
ATTORNEY APPLICATION NUMBER: 07/8794768
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                       Sequence 5, Application US/08466151
| Patent No. 6037453
| GENERAL INFORMATION:
| APPLICANT: Jardieu, Paula M. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Immunoglobulin Variants CORRESPONDENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P0718P2C1D1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/552-9881
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 130 amino acids
TYPE: Amino Acid
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47.92%
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89 SerValAspThr 92
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Query Match:
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                                     RESULT 11
US-08-466-151-5
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GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Leonard G.
TTLIANT: Presta, Leonard G.
TTLIANT: Presta, Leonard G.
TTLIANT: Presta, Leonard G.
TTLIANT: PRESTRUE: B0718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-06-14
PRIOR FILING DATE: 1992-06-14
PRIOR FILING DATE: 1992-06-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-06-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-06-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1992-06-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-06-14
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72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
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Conservative:
Mismatches:
Indels:
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2CIDI
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR PILING DATE: 1995-03-15
PRIOR PILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1992-05-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
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US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
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Sequence 5, Application US/09802077

Batent No. 6699472

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C2US

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1992-03-15

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-05-07

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR PILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

LEMEGTH: 130

WUNDER. DATE: 130
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72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrGluAspThr 91
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US-09-802-096-5
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US-09-802-077-5
NUMBER OF SEQ ID NOS:
SEQ ID NO 5
LENGTH: 130
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Pred. No.:
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Pred. No.:
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US-09-802-077-5
                                            TYPE: PRT
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Sequence 83.7. Application US/09471276
; Sequence 83.5. Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT PILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/065,719
; EARLIER FILING DATE: 1998-04-28
; EARLIER FILING DATE: 1999-04-28
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SEQ ID NOS: 1622
; SEQ ID NO 935
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Matches:
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Job time : 32 secs
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92 AlaThrTyrTyrCysAlaTrpVal 99
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66.67$
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ORGANISM: Homo sapiens
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Best Local Similarity:
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, LOCATION: -26..-1
US-09-471-276-835
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Scoring table:

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Sequence 87, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 128, Appl
Sequence 90, Appl
Sequence 90, Appl
Sequence 90, Appl
Sequence 90, Appl
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118, App
2, Appli
2, Appli
43, Appl
60, Appl
66, Appl
72, Appl
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FILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PFS2;
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
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-MODEL=frame+ n.2p. model - DEV=xlp
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-G-Cgn2 1/USFTO_spool p/NOLAN463-3A/runat_04082005_120128_18886/app_query.fasta_1.263
-G-Cgn2 1/USFTO_spool p/NOLAN463-3A/runat_04082005_120128_18886/app_query.fasta_1.263
-DB=bublished Applications AA -QFMT=fastan -SUPFIX=rabb coun62
-LOOPEXT=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=1 - MATEXT=blo soun62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100
-THR MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFMT=pct - NORM=ext - HEAPGIZE=500 - MINLEN=0
-MAXLEN=200000000 - USRE-NOLAN463-3A @CGN 1 1 199 @runat 04082005 120128_18886
-LOOFUGG - DEV TIMEOUT=120 - WARN TIMEOUT=3 - THREADS=1 - KGAPOP=10 - KGAPEXT=0.1
-FGAPOP=6 - FGAPEXT=0.1 - YGAPOP=10 - YGAPEXT=0.1 - DELOP=6 - DELEXT=0.1
                                                                                                                                August 4, 2005, 19:38:05; Search time 105 Seconds (without alignments) 602.328 Million cell updates/sec
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"GGDZ_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*

"GGDZ_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*

"GGDZ_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*

"GGDZ_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*

"GGDZ_6/ptodata1/pubpaa/USO8_NEW_PUB.pep:*

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"GGDZ_6/ptodata1/pubpaa/USO8_NEW_PUB.pep:*
version 5.1.6
- 2005 Compugen Ltd
                                                                                      protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Publication No. US2003022399641

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

FRICH APPLICATION NUMBER: G0/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-61-19

PRIOR FILING DATE: 2001-65-15

PRIOR PPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-15

PRIOR PPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PLING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/210,210

PRIOR APPLICATION NUMBER: 60/210,210

PRIOR APPLICATION NUMBER: 60/212,210

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PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210
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Conservative:
Mismatches:
Indels:
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80.79%
NUMBER OF SEQ ID NOS: 3239; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 1321; LENGTH: 249
                                                                       TYPE: PRT; ORGANISM: Homo sapiens
US-09-880-748-1321
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US-10-293-418-1321
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Sequence 12, Application US/10898408

Sequence 12, Application US/10898408

Publication No. US20050058642A1

GENERAL INFORMATION:
APPLICANT: GALIBERT, Laurent J.
APPLICANT: TAN, Wei
TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REFERENCE: 3467-A

CURRENT FILING DATE: 2004-07-23

PRIOR FILING DATE: 2003-07-25

NUMBER: OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.2

SEQ ID NO 12

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; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1321
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ORGANISM: homo sapiens
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CORGANISM: Homo sapiens
US-10-293-418-993
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CORGANISM: Homo sapiens
US-09-880-748-954
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/214,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,349

PRIOR FILING DATE: 2001-03-16

PRIOR PRILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VEY: 2.0

LENGTH: DDT
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US-10-293-418-993
; Sequence 993, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.;
; TITLE OF INVENTION: Artibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR PILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
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DELETED1 (1-81) x US-10-898-408-12 (1-115)
                                                                                                                                                                                                                                                                                     ; Sequence 993, Application US/09880748; Publication No. US20030059937Al; GENERAL INFORMATION:
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US-09-880-748-993
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US-09-880-748-954

Sequence 954, Application US/09880748

Sequence 954, Application US/09880748

Publication NO. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITIE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERBNCE: PPS23

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/214,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-17

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NOS: 3239

SEQ ID NO 954
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PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-06-16

NUMBER 0F SEQ ID NOS: 3247

LENGTH: 250
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Publication No. US20030070185A1

GENERAL INPORMATION:
APPLICANT: KUCHERLAPATI, RAJU
APPLICANT: KLAPHOLZ, SUSAN

APPLICANT: MENDEZ, MICHAEL J.
APPLICANT: GREEN, LARRY

APPLICANT: ATALOGOMEN AND APPLICANT: ATALOGOMEN APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: A
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GENERAL INVENTION:

GENERAL INVENTION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFREENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/311,469

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-02-19

PRIOR PILING DATE: 2001-06-15

PRIOR PRIOR APPLICATION NUMBER: 60/233,499

PRIOR FILING DATE: 2001-06-52

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR PRILING DATE: 2000-01-17

PRIOR PRILING DATE: 2000-01-17

PRIOR PRILING DATE: 2000-01-17

PRIOR PRILING DATE: 2000-10-17

PRIOR PRILING DATE: 2000-10-17

PRIOR PRILING DATE: 2000-10-17
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DELETED1 (1-81) x US-09-880-748-954 (1-253)
                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 954, Application US/10293418; Publication No. US20030223996A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Query Match:
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US-10-078-958-2
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TITLE OF INVENTION: PLURAL Wh AND WK REGIONS AND ANTIBODIES PRODUCED TITLE OF INVENTION: THERREROM FILE REFERENCE: CELL 4.18 CON GURRENT APPLICATION NUMBER: US/10/078,958 CURRENT FILING DATE: 2002-02-19 PRIOR PILING DATE: 1996-12-03 PRIOR FILING DATE: 1996-12-03 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 2 LENGTH: 80
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Matches:
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Sequence 40, Application US/10194975

Publication No. US20030039649A1

GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE BEERERCE: 501231.01

CURRENT APPLICATION NUMBER: US/10/194,975

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 40

LENGTH: 97
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CORGANISM: Homo sapiens
US-10-194-975-40
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ORGANISM: Homo sapiens
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RESULT 13

US-10-032-423A-87

US-10-032-423A-87

Sequence 87, Application US/10032423A

Publication No. US20040002450A1

GENERAL INFORMATION:

APPLICANT: BIO-Technology General Corp.

TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: WOMBER: US/10/032,423A

CURRENT PEDLICATION NUMBER: US/10/032,423A

CURRENT PEDLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2001-12-31

PRIOR FILING DATE: 2041-12-31

PRIOR FILING DATE: 2041-12-31

PRIOR FILING DATE: 2041-12-31

PRIOR FILING DATE: 2041-12-31

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 97

TYPE: PRT
                                                    Sequence 87, Application US/10029988B
Publication No. US20040001839A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
TITLE OF INVENTION: WOMER: US/10/029, 988B
CURRENT APPLICATION NUMBER: US/10/029, 988B
CURRENT FILING DATE: 2001-12-31
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PRESEQ for Windows Version 3.0
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CORGANISM: Homo sapiens
US-10-029-988B-87
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69 ---IleSer 70
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Best Local Similarity:
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Pred. No.:
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LENGTH: 97
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Publication No. US20040001822A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/44
CURRENT APPLICATION NUMBER: US/10/032,037B
CURRENT PELICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-31
PRIOR FILING DATE: 2000-12-29
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Matches:
Conservative:
Mismatches:
Sequence 83, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE COF INVENTION: HYBRID ANTIBODIES
FILE REPERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE:
CURRENT FILING DATE:
SOFTWARE: PatentIn version 3.1
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SOFTHARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 97
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Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: human
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US-10-032-037B-87
                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
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                                                                                                                                                                                    SEQ ID NO 83
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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US-10-029-926B-87

US-10-029-926B-87

Sequence 87, Application US/10029926B

PUDLICATION NO. US20040073011A1

APPLICANT: HAGAY, et al.

TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY

FILE REPRENCE: 107934/50

CURRENT APPLICATION NUMBER: US/10/029,926B

CURRENT FILING DATE: 2001-12-31

PRIOR FILING DATE: 12/29/2000

NUMBER OF SEQ ID NOS: 203

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
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Matches:
Conservative:
Mismatches:
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US-10-453-698-83
US-10-453-698-83
Sequence 83, Application US/10453698
Sequence 83, Application US/10453698
PUBLICANT NO. US20040038308A1
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFRENCE: 82 CIP (1089-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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ORGANISM: Homo sapiens
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ORGANISM: human
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Db 50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69

Db 69 ---IleSer 70

Search completed: August 4, 2005, 19:56:40

Job time: 107 secs
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Perfect score:

Sequence:

OM nucleic

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Scoring table:

Total number Minimum DB Maximum DB

Searched:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Roseidues: 1.97 **WEN>
A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <!MM>
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 S44114
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S30529
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S78055
G1HUH2
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B24672
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$38718
$26906
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-MODEL-frame+ n.D2p.model - DEV=X1p
-Q-/CGDT2 1/USFTQ spool p/NOLAN463-3A/runat 04082005 120125 18808/app_query.fasta_1.263
-Q-/CGDT2 1/USFTQ spool p/NOLAN463-3A/runat 04082005 120125 18808/app_query.fasta_1.263
-DB=PIR -QFMT=fastan - SUFPIX==pr -MIRMATCH=0.1 -LOOFCL=0 -LOOPEXT=0
-UNITS=bits -START=1 - TMATRIX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-OUTPMT=pto - NORM=SX - HEAPSIZE=500 - MINENEO - MAXLEN4200000000
-UNFR-NOIAN463-3A @CGN 1 1 63 @runat 0408205 120125 18808 - NCFU=6 - ICPU=3
-NO WMAP -LARGEQUERY - NEG SCORES=0 - WAIT - DSPELOCK=100 - LONGLOG
-DEV TINEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPOFET=0.1 - YGAPOP=6
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1 GAAATCAATCATAGTGGAAG......ATATTAGCAGCTGGTTAGCC
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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S26898
S26805
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Ygapop 10.0 , Ygapext
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Database

Result

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Fri Aug

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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 837454
R;McInter 83.7 Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiAccession: S26805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
A;Reference number: S26800; WUID:92201299; PMID:1348029
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A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                   A;Coss.references: EMBL:X56364
A;Experimental source: V(H)4.2
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < IMM>
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A;Status: translation not shown
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Best Local Similarity:
                               A; Molecule type: DNA
A; Residues: 1-97 <SAN>
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S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 1992
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of VA;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26898
A;Accession: S26898
A;Residues: 1-97 < rTOM-A;Residues: 1-97 < rTOM-
                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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                               Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment) C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Accession: S78052
A;Accession: S78052
A;Residues: 1-140 cHAR>
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A;Reference number: $23716; MUID:92031262; PMID:1718404

A;Accession: $23717

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A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bir A;Reference number: 847009
A;Accession: 847010
A;Accession: S47010
A;Accession: Preliminary
A;Molecule type: mRNA
A;Residues: 1-126 cMAH>
A;Residues: 1-126 cMAH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (RAMOS) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C; Accession: PS0341
R; Ratech, H.
Bjochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A; Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell A; Reference number: PS0341; MUID:92171937; PMID:1540170
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A;Residués: 1-133 <RAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-38/Region: framework 1
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Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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JL0047

JL0047

Ig heavy chain V region precursor (clone cR18) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 16-Aug-1996
C;Date: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5
A;Motecule type: mRNA
A;Motecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V4.21-UniqueD-J5 region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Decies: 3-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accesion: S47010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E. submitted to the EMBL Data Library, July 1994
          A,Reference number: S37453
A,Accession: S37454
A,Status: preliminary
A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Residues: 1-106 <MCI>A,Cross-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: immunoglobulin
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---IleSer 78
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---IleSer 48
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Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C,Accession: B23746
R,Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A,Title: Them 266, 2836-2842, 1991
A,Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RiSanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4064, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
C;Accession: G34964
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A,Residues: 1-97 <SAN>
A,Cross-references: UNIPROT:Q8WUX4; GB:M26998
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heteroterramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                 A,Wolecule type: protein
A,Reaidudes: 1-231 <1ED.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <1MM>
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Conservative:
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B49028
Ig heavy chain V-IV region - human (fragment)
C;Specias: Homos sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuuz
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028
A;Reterence number: A49028, MUID:92008140; PMID:1915549
A;Accession: B49028
A;Status: prelliminary
A;Molecule type: mRNA
A;Residues: 1-143 <TINA
A;Residues: 1-143 <TINA
A;Residues: 1-143 <TINA
A;Experimental source: X-linked agammaglobulinnemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin P;15-97/Domain: immunoglobulin homology <IMM>
C;Accession: A49045
R;Grillot-Courvalin, C; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma Bur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i blancerence number: A49045
A;Reference number: A49045
A;Reterence number: A49045
A;Accession: A49045
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-129 < HAW>
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S14474
Ig heavy chain V region - human
C;Species: Home sapiens (man)
C;Dete: 20-Peb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Date: 20-Peb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S14474
R;van Es, J.H.; Gmelig Meyling, P.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Scatus: preliminary
A;Molecule type: DNA
A;Scatus: preliminary
A;Residues: 1-97 - ESJ3
A;Cross references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:g1335354
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <INM>
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: $26905, $12419
S;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: $26885, MUID:93021117; PMID:1404388
A;Accession: $26905
A;Status: preliminary
A;Moccule type: DNA
A;Cross-references: EMBL:212370; NID:932960; PIDN:CAA78240.1; PID:g32961
A;Residues: 1-98 <TOM>A;Cross-references: EMBL:212370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: $09421; MUID:90059975; PMID:2511001
A;Accession: $132419
A;Scatus: preliminary; translation not shown
A;Rosidues: 1-98 <SAN>
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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CiSpecies: Homo sapiens (man)
CiDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
CiAccession: S44114
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
RiHawkins, R.E.; Zhu, D.; March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       orany chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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Q8Z0Z7
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Q926KS
YBXO, ARATH
YBXO, ARATH
Q6HH50
Q6HH58
Q813F9
Q66AZ3
Q8ZB26
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-MODEL=frame+.ndp.model -DEV=Xlp
-MODEL=frame+.ndp.model -DEV=Xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463_3A/runat_04082005_120125_18797/app_query.fasta_1.263
-Q=/cgn2_1/USPTO_spool_p/NOLAN463_3A/runat_04082005_120125_18797/app_query.fasta_1.263
-DBO_ALIGNE_100 -TRR_SCORE=pct -THR_NATRIX=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=100 -THR_NIN=0 -LAIGN=15 -MODE=LOCAL
-ODCALLIGN=200 -THR_SCORE=pct -THR_NATRIX=0 -THR_NIN=0 -LAIGN=15 -MODE=LOCAL
-OUTFWT=pcc -NORM=ext -HRAFSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER=NOLAN46-3A_@CGN_1 1 244 @runat_04082005_120125_18797 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGG_SCORES=0 -WAXIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THRRAD3=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELDY=6 -DELEXT=0.1
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using frame_plus_n2p model
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TISSUE-Hodgkin lymphoma;
TISSUE-Hodgkin lymphoma;
Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R., Hansmann M.L., Brauninger A.; Hansmann M.L., Brauninger A.; Bubl/GenBank/DDBJ databases.
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564425; CAD92032.1; -.
HSSP, P18523, 1KCV.
InterPro; IPR00110; Ig-like.
InterPro; IPR001596; Ig-v.
SWART; SM00406; IG-v.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CE3D8A846616C908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
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6
                                                                                                                             01-0cT-2003 (TrEMBLrel. 25, Created)
01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0LMAR-2004 (TrEMBLrel. 26, Last annotation update)
Rearranged VH4-34 V gene segment (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                       116 AA
ALIGNMENTS
                                                                                       PRT;
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GATATTAGC

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Q6GMX5
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                                                                                    RESULT 3
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50 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BO19235, AAH19235.2;
PIR; G34964; G34964.
HSSP; P01861; 1ADQ.
Pfam; PF07654; C1-set; 4.
SMART; SM00409; IGG; 2.
SWART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 protein.
595 AA; 65290 MW; 0D4B50776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                     595 AA
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Matches:
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
                                                                                                                                                                                        Created)
                                                                                                                                                     PRT;
                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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66.00%
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                                                                                                                                                     PRELIMINARY;
                                                                          ---IleSer 70
                                                                                                                                                                                                                                   Hypothetical protein.
Homo sapiens (Human).
                                                   61 GATATTAGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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DB:
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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGGTCTCTCAAGAGTCGGGCGAGTCAG 60

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A WEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Tooshyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Tooshyuki S., Carninci P., Prange C.,
A Ras S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Ras S.S., McWam P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
A Fahey J., Helton B.K. Ketteman M., Madda A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Briting M. Madan A., Young A.C., Shevchenko Y., Boutferd G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A T., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO73767; AAH73767.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.-Ix.
R InterPro; IPR003506; Ig.-WHC.
R InterPro; IPR003506; Ig.-WHC.
R InterPro; IPR003506; Ig.-WHC.
R Pfam; PF00047; ig.; 4.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00400; IG; 1.
R SMART; SM00406; IGV; 1.
R PR03ITE; PS50835; IG.LIKE; 5.
R PR03ITE; PS50835; IG.MIKR; 3.
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                                                                                                                                                                  OS-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci. U.S.A. 99:16899-16903(2002).
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Mismatches:
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                                                                                                                    597 AA.
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Matches:
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                                                                                                                    PRT;
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                                                                                                                    PRELIMINARY;
---IleSer 96
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                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altsucherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A blokins R.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A bloatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,
A bloatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,
A bloatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,
A bloatchenko L., Marusina K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Bosak S.A., McEwan P.J., McKernan K.J., Mallahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nollalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Nollalon D.K., Muzny D.M., Green E.D., Dickson M.C.,
B Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A hones S.J., Marra M.A.;

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B and Marra M.A
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01861; IADQ.
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Indels:
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InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig MHC.
Pro; IPR003596; Ig v.
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                                                                                                                      61 GATATTAGC 69
                                                                                                                                                                                              ---IleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGHM protein.
Homo sapiens (Human).
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Fedingold E.A., Grouse L.H., Derge J.G.,
Aluenner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Staplecon M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Hely J., Helton E., Ketteman M., Madan A., Yourigues S., Sanchez A.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Milting M. I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Marker M. Marker M.A.,
Marker M.A.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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C TISSUE-Lymph;

A Strausberg R.;

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

IL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.)

R EMBL; BC017356; AAH17356.2; -..

BR PIR; SISS90; SISS90.

BR HASP; P01861; 1ADD.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003599; Ig.

DR SWART; SM00409; Ig.

DR SWART; SM00409; IG.; 2.

DR SWART; SM00409; IG.; 2.

DR SWART; SM00409; IG.; 1.

DR SWART; SM00409; IG.; 1.

DR PROSITE; PSS00839; IG LIKE; 5.

DR PROSITE; PSS00839; IG LIKE; 5.

DR PROSITE; PSS00839; IG LIKE; 5.

DR PROSITE; PSS00839; IG LIKE; 5.

DR PROSITE; PSS00839; IG LIKE; 5.

DR PROSITE; PSS00839; IG LIKE; 5.
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Homo sapiens (Human)
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                                                 RESULT 5
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DELETED1 (1-81) x Q96AA6 (1-625)

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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60 

Gaps:

DELETED1 (1-81) x Q9BU10 (1-597)

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1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60

GATATTAGC 69

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RESULT 7
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                                                                                                                                                                                TISSUE=Muscle;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJUSTER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

A Distchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Cappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Pahey J., Helton E., Ketteman M., Madan A.M., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

K Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

R "Generation and initial analysis of more than 15,000 full-length human
76 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 94
                                                                                                                                                                                                                                                                                                        IGHM protein.
Homo saplens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBU databases.
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
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10 098088
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RY SUGENCE FINDING.

RY ENCORAGE ENDING.

RY TISSUB-Primary B-Cells;

RY STREEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B.B., Budgner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Jezeberg B.B., Buccow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RY Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RY Hallalon D.K., Maruny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

Ry Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human

RT Grouss CDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                         Dolaco sapiema (menana).
Eukarda: Metazona: (hordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063384; AAH63384.1; -.
HSSP; P01820; 1A7N.
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PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                        576 AA.
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Matches:
                                                                                                                                                                                 Created)
                                                                                                                        PRT;
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003506; Ig_v.
Pfam; PF007654; Cl-set; Z.
Pfam; PF00767; ig; l.
SMART; SM00407; IG; l.
SMART; SM00407; IGC1; 3.
                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0371
84.40
70.37%
66.67%
                                                                                                                        PRELIMINARY;
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TISSUE=Primary B-Cells;
---IleSer 89
                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                             protein.
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                                                                                                                                                                                                                                                                                                             Name = IGHD:
88
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                                                                                                                                                     Q6P4I8;
                                                                                                                        Q6P4I8
                                                                                                                                                                                                                                                                             IGHD
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DELETED1 (1-81) x Q6P4I8 (1-576)

1 GANATCANTCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60 

69

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(1-81) x Q6GMX7 (1-477)

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90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109
99
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
15-JUJ-1999 (Rel. 1 region ARH-77 precursor.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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D segment.
J segment.
By similarity.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                            ---AGCAGCTGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA
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Pfam; PF00047; Ig; 1.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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78.40
66.67$
62.96$
56.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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146
115
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                                                                                                                                                                                                                                                                                                                                64 ATT-----
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SEQUENCE
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DB:
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---IleSer 90

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Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6GMX6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 ValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 ----- 57
                                       01-JUN-2003 (TrEMBLrel. 24, Created)
-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSOBL004YM19 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=mix FVB/N; TISSUE=Mammary tumor; MEDLINE=2388257; PubMed=1247932; DOI=10.1073/pnas.242603899; MEDLINE=2388257; PubMed=1247932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Sthauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGT---
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Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CAGGATATTAGCAGC
                                                                                                                                                                                                                                                                                       TISSUE-B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX2300; CAD62627.1; -.
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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Mismatches:
Indels:
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PROSITE; PS50835; IG_LIKE; 1.
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PRELIMINARY;
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                    286SX2;
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90 ArgAspThrSerLysAsnGlnPhePheLeuLysLeuAsnSerValThrThrGluAspThr 109
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Shevchenko Y., Souffard G.G. Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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TISSUE-Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2238827; PubMed=12477932; Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
HSSP; P01820; 1G7J.
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479 AA, 51992 MW, 768E39A138918892 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Conservative:
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP07654; C1-set; 2.
SMART; SM00406; IGV; 1.
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Best Local Similarity:
Query Match:
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TISSUE=Hybridoms;
MEDLINE=9621465; PubMed=8648670;
MEDLINE=9621465; PubMed=8648670;
Staheen F., Duan L., Zhu M., Bagaara O., Pomerantz R.J.;
"Targeting human immunodeficiency virus type 1 reverse transcriptase by intracellular expression of single-chain variable fragments to inhibit early stages of the viral life cycle.";
EMBL; U40716; AAB64342.1; -.
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
D. Latchenko. L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.M., McMerlan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
Jones S.J., Marra M.A.,
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
REMBL, BC073766; AA473766.1; -
REMBL, BC073766; AA473766.1; -
RINTERPORT IPRO03599; Ig -1.
RINTERPORT IPRO03599; Ig -1.
RINTERPORT IPRO03069; Ig MHC.
RINTERPORT IPRO03069; Ig WHC.
RINTERPORT IPRO03596; Ig WHC.
REMM: PF07654; C1-set; 3.
REMM: SMOA409; IG; 2.
REMM: SMOA409; IG: 1.
REMM: SMOA409; IG: 1.
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Last annotation update)
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzuy D.W., Sodergren B.J., Lu K., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
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25-OCT_2004 (TrEMBLrel. 28, Last sequence update)
25-OCT_2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
Anti-HIV-1 reverse transcriptase single-chain variable.
Eukaryota: Metazoa (Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae
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REMBL, BCO11857, AAH11857.2; ...
RISESSO, SISSOO, SISSOO, SISSOO, IGTON, INTERPRO, IPRO01359; IGTON, INTERPRO, IPRO01359; IGTON, INTERPRO, IPRO01359; IGTON, INTERPRO, IPRO01356; IGTON, INTERPRO, IPRO01356; IGTON, INTERPRO, IPRO01356; IGTON, INTERPRO, IPRO01356; IGTON, INTERPROSITE; PSSO0356; IGTON, INTERPROSITE; PSSO0356; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, IGTON, INTERPROSITE; PSSO0359; IGTON, INTERPROSITE; PSSO0359; IGTON, IGTON, INTERPROSITE; PSSO0359; IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTON, IGTO
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TISSUE=Primary B-Cells;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
Homo sepient).
Homo sepiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
[11]
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Cilin. Immunol. Immunopathol. 87:184-192(1998).

EMBL; AF035041; AAD56277.1; -.

PIR; PH0876; PH0876.

PIR; S12416; S12416.

HSSP, P01820; 1G7J.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

SMART; SM00406; IGV.

SMART; SP50835; IG_LIKE; 1.
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.-c.
InterPro; IPR003596; Ig.-c.
InterPro; IPR00409; Ig.-c.
SNART; SN00409; IG.2.
SNART; SN00408; IGC2; 2.
RNART; SN00408; IGC2; 2.
RNART; SN00408; IGC2; 2.
RNART; SN00408; IGC2; 2.
RNART; SN00408; IGC2; 2.
RNART; SN00408; IGC2; 2.
RNART; SN00408; IGC2; 2.
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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119 AA; 13219 MW;
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Search completed: August 4, 2005, 19:37:58 Job time : 113 secs

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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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ADA89266
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2001US-0276248P.
2001US-0277379P.
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25-MAY-2001;
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16-MAR-2001;
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 Command line parameters:
-MODEL=frame+ n2p.model - DEV=Xlp
-0=/Cgn2_1/USF7PC spool_p/NOLAN463-18P/runat_04082005_120453_19604/app_query.fasta_1.263
-0=/Cgn2_1/USF7PC spool_p/NOLAN463-18P/runat_04082005_120453_19604/app_query.fasta_1.263
-0B-A_Geneseq -0FMT=fastan - SUPPIX=x=g - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0
-UNITS=bits -START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-UNITS=bits -START=1 - END=-1 - MATRIX=100 - TRANS=human40.cdi - LIST=45
-OTFRYT=ptc - TRR_EXCRE=pct - THR_MAX=100 - TRANS=NOCO000000
-USER=NOLAN463-3B @CGN 1 1 224 @runat_04082005 120453_19604 - NCPU=6 - ICPU=3
-NO_WMAP - LARGEQUERY - NGG = GCORES=0 - WAIT - DSPBECCK=100 - LONGICG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPOP=6
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Abg78212 Human Fv
Abg91903 Human ant
Abc27107 Human ger
Adb75646 Human pro
Add28104 Lymphoma
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1 CGGGCGAGTCAGGATATTAG.....ACAACCCGTCTCTCAAGAGT
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                    protein search, using frame_plus_n2p model
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                       diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and acquired immunodeficiency common variable immunodeficiency and acquired immunodeficiency syndrome (AIDS)). ABB43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                This invention describes novel antibodies that immunospecifically bind to
                                                                                                                          Blymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiADS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain antibody that immunospecifically binds BLyS SeqID 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; Bcall proliferation; differentiation; scFv, myasthenia gravis; multiple sclerosis, asthma; rheumatoid arthritis; ADS; leukaemia; carcinoma; lymphoma; antirheumatic; antiathritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 Vaughan T, Hilbert
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Conservative:
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                                                                                        Claim 1; Page 1993-1994; 3148pp; English.
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 Choi GH.
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Barash SC,
                         WPI; 2002-114799/15.
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Best Local Similarity:
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1343 and encodes a protein that is a member of the tumour corrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFv8) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysathenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and cutivities such as antirheumatic, antiathering cand cytostatic. This activities such as antirheumatic, antiathering cand cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format con the printed specification, but was obtained in electronic format.
                                                                                                                                                                                                                                                                                                   Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                                                                                                                  Hilbert
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16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                                 (HUMA-) HUMAN GENOME SCI INC
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immunoglobulin; Ig; heavy chain variable domain; light chain variable domain; major histocompatibility complex; MHC; gpl00; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;

cancer.

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The present invention describes a protein comprising an immunoglobulin (1g) heavy chain variable (VH) domain and an Ig light chain variable (VL) domain. The protein blinds a complex comprising a major histocompatibility complex (WHC) and a peptide, does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide in the absence of the MHC. The peptide is a peptide fragment of gp100, MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition comprising one or more nucleic acids for expressing the Ig that binds a complex having an MHC and a peptide, does not substantially bind the comprising one or more nucleic acids for expressing the Ig that binds a comprising an ence of the MHC; (3) an isolated nucleic acid comprising a first segment that encodes the Ig variable domain; (4) a comprising a first segment that encodes the Ig variable domain; (4) a comprising a first segment that encodes the complex acid sequences that encodes the novel protein; (5) a transgenic animal whose genome includes heterologous nucleic acid sequences that encode the protein; (6) identifying the protein that specifically binds the MHC-peptide complex; (7) expressing an antigen-binding protein; (8) ablating or killing a target cell that a complex in a sumplect, and (10) detecting an MHC-peptide complex in a sample. A protein of the invention has cytostatic activity, and can be used in gene therapy. The protein is useful for preparing a composition for treating or preventing a composition for treating or preventing a composition for treating or preventing a composition for treating or preventing a composition for treating or preventing a composition for treating or preventing a composition for treating or preventing a peptide complex where the peptide component in as peptide an MHC-peptide complex where the peptide component in a septime therapent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.
                                                                                                                                                                                                                                                                                                                                                                                              (DYAX-) DYAX CORP.
(TECR ) TECHNION RES & DEV FOUND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 28B; 224pp; English.
                                                                                                                                                                                                                                                                                                    20-FEB-2003; 2003WO-US005128.
                                                                                                                                                                                                                                                                                                                                                     20-FEB-2002; 2002US-0358994P.
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99.90
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                                                                                                                                                                                                            WO2003070752-A2.
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                                                                                                                                                                Homo sapiens.
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                                                                                                                                        Synthetic
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125
22
1
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2
1
1
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                        3 GGCGAGTCAGGATATTAGCAGC-
                                                                    DELETED2 (1-81) x ADA89274 (1-125)
                  50.00%
47.83%
71.36%
                               Best Local Similarity:
                    Percent Similarity:
                                       Query Match:
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24

26 GlyGlySer----ileSerSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44

셤

transgenic Xenomice, created using the method of the invention. The specification describes a transgenic non-human mammal which has genome modifications that comprise an inactivated endogenous immunoglobulin [Ig] locus, so that the mammal does not display normal B-cell development. The modified genome also has an inserted human heavy chain Ig locus in germline configuration, the human heavy chain Ig locus in germline configuration, the human N-H genes and an inserted human J-H genes, and human D-H genes, human D-H genes, and human V-H genes and an inserted human kappa light chain Ig locus comprising a human kappa constant region, J-kappa genes, human Ig locus comprising a human kappa constant region, J-kappa genes, including both a multiple chain layer and V-kappa genes inserted are selected to restore normal B-cell development in the mammal. The transgenic animals have a near complete human Ig locus, including both a human heavy chain locus and a human kappa light chain locus. They can be used for the production of human antibodies when exposed to particular antigens e.g. when exposed to human antibodies when exposed to particular antigens e.g. when exposed to human antibodies when exposed to particular will produce antibodies to IL-8, EGFR or INF- alpha respectively Human; immunoglobulin; Ig; transgenic; non-human mammal; inactivated endogenous Ig locus; B-cell development; Muman heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene; kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa; production; antibody. New transgenic non-human mammals - having an inactivated immunoglobulin locus and a near complete human immunoglobulin locus, used for production of human antibodies. 7 64 Mendez M, 3578 Amino acid sequence of a human antibody fragment. Length: Matches: Conservative: Mismatches: Klapholz S, Disclosure; Page 71; 128pp; English. AAW62794 standard; peptide; 80 AA Kucherlapati R, 97WO-US023091 96US-00759620 0.000334 98.20 65.62% 59.38% (first entry) 81 67 WPI; 1998-333314/29. (ABGE-) ABGENIX INC. rLeuLysSer Percent Similarity: Best Local Similarity: Sequence 80 AA; Jakobovits A, 03-DEC-1996; Homo sapiens. 03-DEC-1997; WO9824893-A2 23-SEP-1998 11-JUN-1998. Alignment Scores: Pred. No.: AAW62794; 64 72 RESULT 4 AAW62794 g 셤 ò ð

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Multiple sclerosis patient CSF B-cell VH region (clone 4d76)
                                                                                                                                                                                       Multiple sclerosis; cerebrospinal fluid; CSF; B-cell; heavy chain variable region; VH gene; somatic hypermutation; B-cell clonality; RA gene; diagnosis; human.
80
                                                                                                                                                                                                                                                                                                                           note= "replaces Gly of RA"
                                                                                                                                                                                                                                                                                                                                                           RΑ"
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                                                                                                                                                                                                                                                                                          note= "replaces Glu of RA"
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                                                                                                                                                                                                                                                                                                                                                                                           Gly of RA"
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Gaps:
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/label= CDR1
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'label= CDR2
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/label= FR2
                        DELETED2 (1-81) x AAW62794 (1-80)
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/label= FR3
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/label= FR1
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70.14%
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Query Match:
DB:
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Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                  in nucleotide and predicted amino acid (see AAYOG691-94) sequences were compared with the closest known germline VH genes; for 4d76, this was RA. The results provided direct evidence that intrathecal clonally expanded Brecalls from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that havd undergone antigen selection. This finding implicates an important pathogenic pathway for the development of demyelination in CNS of MS. The invention provides assay kits for determining Becall or T-cell clonality. This technology cells in the CNS of patients, which is important for further understanding of the role of antigen(8) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy
                                                                                                                                                                                                                          This sequence represents a heavy chain variable region (VH) as predicted from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of B-cell clonality by amplification or enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Fv molecule hypervariable region related peptide #87.
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Matches:
Conservative:
Mismatches:
Indels:
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97CA-02216595.
97CA-02220245.
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65.62%
59.38%
70.14%
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                                                                                                        WPI; 1999-276985/23.
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                                                                                                                      N-PSDB; AAX25318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97 AA;
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 19-SEP-1997;
04-NOV-1997;
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                                             NIO (/KNIO)
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                                                                                                                                                                     digestion
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11-JUL-2002.
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                                                                                                                                                                                                             The invention relates to a peptide or polypeptide comprising an FV molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and FV is a single chain FV (scFV) or a disulfide FV (dsFV). The peptide, optionally in association with or attached, complied, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, asrcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer composition for use in inhibiting the growth of a diseased or cancer composition for use in inhibiting the growth of a diseased or cancer coll. This sequence represents a human FV molecule hypervariable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leuksemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                          Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
                                                             Guy R, Lipschitz O, Szanton E, Levanon A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
119
2
3
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Matches:
Conservative:
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                                     (BIOT-) BIO-TECHNOLOGY GEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.000353
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65.62%
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                                                             Lazarovits J,
Peretz T;
                                                                                                  WPI; 2002-619166/66
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97 AA
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Pred. No.:
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                                                             Hagai Y, L
Plaksin D,
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DB:
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ABG91903
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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenceis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia of tumour or leukaemia cells, increase in number of tumour or leukaemia of diseased cells to damage by anti-disease, anti-cancer or anti-cleukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for disanosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases mediated by abnormal platelet cumopathic diseases and other diseases mediated by abnormal platelet cuntonin and diseases caused by sulphated tyrosine-dependent protein-contein interactions. This sequence represents a human antibody fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                       Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 GlyLys----GlyLeu----GluTrplleGlyGlulleAsnHisSerGlySerThrAsnT
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Levanon A;
                                                                                                                                                                            Mar-Haim
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Peretz T,
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Kooperman L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 269; Opp; English.
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31-DEC-2001; 2001WO-US04942
                                                 2000US-00751181
2000US-0258948P
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                                                                                                                                                                          , Hagai Y,
Richter T,
                                                                                                                                                                                                                                                     WPI; 2002-674776/72.
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Query Match:
DB:
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                                                                                                                                                                            Lazarovits J,
                                                 29-DEC-2000;
29-DEC-2000;
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                                                                                                                                                                                                      Szanthon E,
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Fri Aug

04-DEC-2003 (first entry)

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The invention describes a meribod of mananistic antibody.

Comparising making chimmeric antibodies contraining a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis of selection, for humanisation. The method is useful for making a humanised antibody sequence of any subject species to a less converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support on human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparison framework sequences between non-human and human antibodies. This sequence represents a human heavy chain variable region gene segment used in the
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                                                                                                                                                                                                                                                                                                                                                                Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes a method of making a humanised antibody,
Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 1; 31pp; English
                                                                                                                                                                                   12-JUL-2002; 2002US-00194975
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                                                                                                            US2003039649-A1
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Best Local Similari
                                                                                                                                                                                                                                                         (FOOT/) FOOTE
                                                                            Homo sapiens.
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The invention relates to a novel artificial single-stranded antibody library with superior-repertory. The library is created by using a CDNA library as template for amplifying a fragment containing the CD1 and CD2 regions of the VH or VL region of immunosolbulin gene and a fragment containing the CD3 region by PCR, respectively, producing VH and VL libraries, transferring into a host, and displaying the single-stranded antibody on a phase surface. An antibody library of the invention is useful as a tool in proteomics and antibody chips and filters, for screening ligands for antigens, and for studying protein-DNA interaction, diagnosis and treating various diseases. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Highly stable artificial antibody libraries with super-repertory and little contamination from unexpressible ones, useful as tool in proteomics and e.g. for diagnosis and treating various diseases.
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                                                              antibody library, CD1 region; CD2 region; VH region; VL region; immunoglobulin; CD3 region; TM1 scFv; human.
                                      Human protein relating to the invention SEQ ID NO:55
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                   22-NOV-2001; 2001JP-00358602
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                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                     The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (l) treating a patient suffering from or at risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor inhibiting glycosylation of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (s) has cycostatic activity, and can be used in gene therapy, and as a glycosylation inhibitor. The method is useful in classifying a B-cell as malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence represents an Ig variable region sequence which is used in the cycostation of the present invention.
                                                                                                                                                                                                                                         Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; non-Hodgkin's lymphoma.
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Conservative:
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                                                                                                                                                 07-MAR-2002; 2002GB-00005395.
                                                                                                                           24-FEB-2003; 2003WO-GB000783
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Best Local Similarity:
                                                                             WO2003074059-A2.
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                                             Synthetic.
Homo sapiens.
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody especially the stability, or antigen blinding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody may be variable region sequence used to illustrate the invention.
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variable
                                              Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dahiyat B;
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VEGF antibody heavy chain variable region VH_4-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Fig 16a; 135pp; English
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29-MAY-2002; 2002US-0384197P.
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                                                                                                                         Homo sapiens
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variable region; human.
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                                                                                                                                                                                                                                                                                                                                                                                                      physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position (s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical property. The method is useful for optimizing solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to a method for optimizing at least one
                                                                                                                                                                                                                                                                                                        antibodies
variable
Antibody, stability, solubility, antigen binding affinity, variable region; human.
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Matches:
Conservative:
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                                                                                                                                                                                                                                                 Desjarlais JR, Marshall SA,
                                                                                                                                                                                                                                                                                                                                                                  Example 16; Fig 40a; 135pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 yrAsnProSerLeuLysSer
                                                                                                                                              03-MAR-2003; 2003WO-US006598.
                                                                                                                                                                         01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
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Query Match:
                                                                                    WO2003074679-A2
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                                                                                                                                                                                                                   (XENC-) XENCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2004
                                                                                                                  12-SEP-2003
                                                                                                                                                                                                                                                 Lazar GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least noe antibody sequence with at least optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody especially the stability, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody way be variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||::: ||| GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybrid antibody; antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable
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Matches:
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                                                                                                                                                                                                                                                                                                                                                             Marshall SA,
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                                                                                                                                                                                                                      01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                                                              03-MAR-2003; 2003WO-US006598
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                                                                                                                                                                                                                                                                                                                                                             Lazar GA, Desjarlais JR,
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                                                    WO2003074679-A2
                                                                                                                                                                                                                                                                                                        (XENC-) XENCOR.
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Homo sapiens
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**EXEXEXEX** 

18-SEP-2000 (first entry)

AAB01949;

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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FRI, FRZ, FRZ and FR4; (iv) comparing the sequence of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a crarget species; (v) selecting a second component to sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component sequence from the group consisting of FRI, FRZ, FRZ and FR4; (vi) comparing the sequence of the second component sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (vii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and antibody or the second component and antibody or sequences to one or more complementarity determining regions (CDRS) of the initial antibody, to produce a hybrid antibody or hybrid antibody fragment (claimed). The antibody and antibody fragment. The method is useful for producing a hybrid antibody fragment for the representations of the produces of the core in the core in the core in the core in the core of the core of the core in the core of antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that minital antibody endianced immunogenicity while minital antibody and antibody and antibody fragment. The method is useful for the second component and exhibit antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that minital antibodies and exhibit reduced immunogenicity while the content the content of the content and exhibit antibodies and exhibit reduced in the content and exhibit and the content of the content
                                                                                                                                                                                                                                                                                                                                            Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the VH gene locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 83; 77pp; English
                                                                                                             03-DEC-2002; 2002WO-US038450
                                                                                                                                                           03-DEC-2001; 2001US-0336591P
                                                                                                                                                                                                       (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                 WPI; 2003-513753/48.
                                                                                                                                                                                                                                                     Wu D;
                   WO2003048321-A2
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                                                               12-JUN-2003
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0 8 9 0 8 9 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 0.000353 98.20 65.62% 59.38% 70.14% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: 

DELETED2 (1-81) x ADJ80323 (1-97) 42

61

g ò RESULT 15 AAB01949 ID AAB0 XX

AAB01949 standard; protein; 114 AA

Lymphoid cell line preparation useful for producing gene products having desired activity, involves screening and selecting cells having ongoing target sequence diversification and higher mutation rates. Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M; IgM; V gene diversity; directed constitutive hypermutation; target sequence diversification; terminal deoxynucleotidyl tran TdT; clonal expansion; selection; heavy chain variable region; Anti-Id1 Ab binding-defective mutant Ramos cell VH K70N/S77N, /note= "Encoded by CAG" Sale JE, Neuberger MS, Cumbers SJ; Location/Qualifiers Example 5; Page; 69pp; English. 98GB-00022104. 99GB-00001141. 99GB-00013435. 99WO-GB003358 (MEDI-) MEDICAL RES COUNCIL. 2000-317971/27. Misc-difference 71 N-PSDB; AAA52435 mutant; mutein WO200022111-A1 09-OCT-1998; 19-JAN-1999; 09-JUN-1999; Homo sapiens. Synthetic. 08-OCT-1999; 20-APR-2000

The invention relates to a method of preparing a lymphoid cell line capable of directed constitutive hypermutation of a target capable of directed constitutive hypermutation of a target nucleic acid mutation exceeds that of other nucleic acid mutation for cate of target nucleic acid mutation exceeds that of other nucleic acid mutation exceeds that of other nucleic acid mutation exceeds that of other nucleic acid mutation exceeds that of other nucleic acid mutation by a factor of 100 or more. The invention also relates to a method for preparing a gene product with a desired activity, comprising expressing a nucleic acid encoding the target gene operably linked to a sequence which directs hypermutation e.g., terminal deoxynucleotidyl transferase (TdT), in the lymphoid cell line, and identifying a cell or cells which express a mutated gene product with the desired activity. One or more clonal populations of the identified cells is established, and cells with an improved activity of interest are selected. These steps may be iteratively repeated until a gene product with a desired of the invention are used for directed constitutive hypermutation of a nucleic acid region in the preparation of a gene product, preferably an enzyme or an immunoglobulin (Ig) with a desired activity. In the exemplifications of the invention, IgM-secreting Ramos cells were selected for use as they undergo hypermutation during clonal expansion. This was determined on the basis of the amount of diversity in the heavy chain variable region (VH). Sequences AAB01949-B01954 which have lost the ability to bind anti-idlotype antibodies (anti-Idl Ab) relative to the wild-type VH (AAB01949). Note: The present sequence is not shown in the specification, but is derived to the wild-type VH (AB01949).

Sequence 114 AA;

0.00037 Alignment Scores: Pred. No.:

114

Length:

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	65.62%	65.62% : 59.38%	Percent Similarity: 65.62% Conservative: 2 Best Local Similarity: 59.38% Mismatches: 3 Query Match: 8

DELETED2 (1-81) x AAB01949 (1-114)

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Search completed: August 4, 2005, 20:00:48 Job time: 123 secs

9, App Appli

Run on:

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Sequence 13, Appl
Sequence 837, App
Sequence 79, Appl
Sequence 77, Appl
Sequence 16, Appl
Sequence 16, Appl
                                                                                                                                           Sequence 69, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 39, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
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Sequence 65, Appl
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                                                                                                                        Sequence 169,
                                                                                 Sequence 77,
Sequence 16,
Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-545-809A-118
Sequence 118, Application US/08545809A
Sequence 118, Application US/08545809A
Barent No. 6056878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Mateuda, Fuminiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
                                      sequence
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                   Sequence
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US-08-466-163B-5

US-09-802-095-5

US-09-302-095-5

US-09-372-425A-2

US-09-372-425A-2

US-09-471-276-837

US-08-918-148-79

US-09-138-197-16

US-09-138-197-16

US-09-726-219A-169

US-09-726-219A-169

US-09-726-13B-7

US-09-726-13B-7

US-09-726-13B-7

US-09-726-13B-7

US-09-726-13B-7

US-09-726-13B-7

US-09-126-13B-7

US-09-131-39-6

US-09-131-39-6

US-09-131-39-6

US-09-131-39-6

US-09-131-38-18

US-09-131-18-18

US-09-131-18-18

US-09-177-12B-18

US-09-177-12B-18

US-09-177-12B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
TELEBHONE: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                         US-08-545-809A-140
US-08-851-362D-22
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STREET: 225 Franklin Street
CITY: Boston
  TELEX: 200154
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COUNTRY:
                                      RESULT 1
   Sequence 118, App
Sequence 4, Appli
Sequence 2, Appli
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5, App
Appli
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6, Appli
25, Appl
                                                                               4, 2005, 19:53:13 ; Search time 29.5 Seconds (without alignments) 409.937 Million cell updates/sec
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Sequence 5,
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Sequence 6
Sequence 2
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1 CGGGCGAGTCAGGATATTAG......ACAACCGGTCTCTCAAGAGT
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1: /cgn2_6/ptGdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptGdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptGdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptGdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptGdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptGdata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                           - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-545-809A-118
US-08-793-450-4
US-09-203-768A-2
US-09-372-425A-6
US-09-372-425A-6
US-09-025-769B-25
US-09-490-078-25
US-09-490-153-25
US-09-490-324-25
US-08-545-809A-137
US-08-545-809A-137
US-08-545-809A-137
US-08-545-815
                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                   513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                        Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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26449678631

Result

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Alignment Scores:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARGARITTE CHRISTEL
APPLICANT: MARGARITTE CHRISTEL
APPLICANT: MARGARITTE CHRISTEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: DELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ALLINGTON
STATE: USA
COUNTRY: USA
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ANDERSEENCE/ONCERT UNMBER: E80-118-0 PCT
TELECOMMUNICATION INFORMATION:
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119
22
33
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ACAACCCGTCTCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          4.16e-05
98.20
65.62%
59.38%
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TYPE: amino acid
TOPOLOGY: linear
                                                       LENGTH: 116 amino acids TYPE: amino acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-793-450-4
                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                    US-08-545-809A-118
                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
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US-08-793-450-4
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Sequence 2, Application US/09203768A
Parent No. 6787638
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Of Use
TILE REFERENCE: P. 1X 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 139
                                                                                                                            61 GlyLys----GlyLeu----GluTrpl1eGlyGlu1leAsnHisSerGlySerThrAsnT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: RACACHEK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139
129
3
3
0
 123
119
2
3
8
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                          Gaps:
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                                                                                                    DELETED2 (1-81) x US-08-793-450-4 (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ACAACCGTCTCTCAAGAGT 81
                                                                                                                                                                                                        ; Sequence 8, Application US/08793450; Patent No. 6312690
4.25e-05
98.20
65.62%
59.38%
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98.20
65.62%
59.38%
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, ORGANISM: Homo sapiens
US-09-203-768A-2
                          Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-08-793-450-8
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Query Match:
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRICH APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Sequence 6, Application US/09372425A;
Patent No. 6475749;
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
APPLICANT: Ramon Montano
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELETED2 (1-81) x US-08-793-450-8 (1-472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ACAACCCGTCTCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 472 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.20
65.62%
59.38%
70.14%
                                                                                                                                                                                                                                                                                                                                                   JECUTE 703-2220
TELEPHONE: 703-413-2220
TELEPHONE: 703-413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-793-450-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
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US-09-372-425A-6
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 1lag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plucckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: Heavy chain without Tailpiece - AA
                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
               ATTORNEY AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECOMUNICATION INFORMATION:
TELEPHONE: (310) 788-500
IELEPHONE: (310) 788-5100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-700-1995
ATTORNEY AGENT INFORMATION: NAME: James F. HALEY, Jr., ESQ. REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: MORPHO/5 TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DELETED2 (1-81) x US-09-372-425A-6 (1-429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-025-769B-25; Sequence 25, Application US/09025769B; Patent No. 6300064
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                                                                                                                                                                                                                                                                                                                                                                                                93.20
65.62%
56.25%
66.57%
                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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ADDRESSEE: James F. F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
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Best Local Similarity:
FILING DATE:
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WEDUW TYPE: Floppy disk
COMBUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
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; Sequence 25, Application US/09490070A
; Patent No. 6656248
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
; TITLE OF INVENTIONES: 373
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,298 REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
                                                                                                                                                                                                                                                                                                                     DELETED2 (1-81) x US-09-025-769B-25 (1-118)
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TELEPHONE: (202) 912-2000
INFORMATION FOR SEQ ID NO: 25:
; TELEFAX: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                        0.000291
92.10
50.00%
47.73%
65.79%
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                           Alignment Scores:
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DB:
                                                                                                                                                                                                           Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    3 GGCGAGTCAGGATATTAGCAGC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haley, Jr., Esq.
of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQIENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                              DELETED2 (1-81) x US-09-490-070A-25 (1-118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                  LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. STREET: 1251 Avenue
SEQUENCE CHARACTERISTICS:
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ZIP: 10021
COMPUTER READABLE FORM:
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Ilaq, Vic
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50.00%
47.73%
65.79%
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STATE: New York
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 yLeuGluTrpIleGlydluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TGGTTAGCCGAAATCATAGTGGAAGCACCAACTACAACC
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; Sequence 25, Application US/09490324
; Patent No. 6828422
; Patent No. 6828422
; APPLICANT: Knappik, Achim
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FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 118 amino acids
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Honjo, Tasuku
APPLICANT: Matouda, Pumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STRETT: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
SEQUENCE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06501/004001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REGISCOMMUNICATION INFORMATION:
TELEPONONE: 617-542-5070
TELEPAX: 617-542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                       3 GGCGAGTCAGGATATTAGCAGC-
                                                                                                                                                                                     0.000291
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TYPE: amino acid
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Best Local Similarity:
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64 8Ser 65
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US-08-545-809A-137
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DB:
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RESULT 13
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Sequence 835, Application US/09471276

Sequence 835, Application US/09471276

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Dimas Milne Edwards, J.B.

APPLICANT: Dimas Milne Edwards, J.B.

APPLICANT: Dimas Milne Edwards, J.B.

APPLICANT: Dimas Milne Edwards, J.B.

FILE REFERENCE: GENSET. 025CP1

CURRENT APPLICATION NUMBER: US/09/471,276

CURRENT APPLICATION NUMBER: 09/069,047

EARLIER FILING DATE: 1998-04-28

EARLIER FILING DATE: 1998-04-28

EARLIER FILING DATE: 1998-04-09

NUMBER OF SEQ ID NOS: 1622

SOFTWARE: Patent.pm

SEQ ID NO 835

LENGTH: 147
                                                                                                                                               45 GlyAspSer----IleSerSerGlyAsnTrpIleTrpValArgGlnProProGlyLysGl 63
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Matches:
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                                                                                                     DELETED2 (1-81) x US-08-545-809A-137 (1-120)
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US-08-466-151-5
; Sequence 5, Application US/08466151
                                                                                                                                 3 GGCGAGTCAGGATATTAGCAGC-
           0.000402
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                                  Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                  83 sSer 84
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US-09-471-276-835
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Alignment Scores:
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                                                             Query Match:
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13 LysProSerGinSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:
COMPUTER: 15 inch, 1.44 Mb floppy disk COMPUTER: 15 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
              APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
WUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Svoboda, Craig G.
REGISTARION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELETED2 (1-81) x US-08-466-151-5 (1-130)
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR.1995
BRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN.1994
BRIOR APPLICATION NUMBER: 07/87495
FILING DATE: 07-MAY.1992
BRIOR APPLICATION NUMBER: 07/87495
FILING DATE: 07-MAY.1992
BRIOR APPLICATION NUMBER: 07/87495
FILING DATE: 14-AUG-1991
ATTORNEY/AGRET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGGGCGAGTCAGGATATTAGC
                                                                                                           ADDRESSEE: Generitech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
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Amino Acid
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Best Local Similarity:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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DB:
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US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REPERENCE: P0718P2C305
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US/09/802,077
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1995-03-15
; PRIOR PLILNG DATE: 1994-01-26
; PRIOR FILING DATE: 1992-01-06
; PRIOR FILING DATE: 1992-05-07
; PRIOR FILING DATE: 1992-05-07
; PRIOR FILING DATE: 1991-08-14
; PRIOR FILING DATE: 1991-08-14
; PRIOR FILING DATE: 1991-08-14
; PRIOR FILING DATE: 1991-08-14
; RUMBER OF SEQ ID NOS: 64
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
                                                                                                                                                                                                                                                                                                                                                                     33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrile 52
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Pred. No.:
    US-09-802-096-5
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; Sequence 5, Application US/09802096
; Batent No. 6685939
; General Information:
    APPLICANT: Usenard G.
    TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended; ITLE REFERENCE: P0718P2C3US
    CURRENT APPLICATION NUMBER: US/09/802,096
    CURRENT FILING DATE: 2001-03-08
    PRIOR PILING DATE: 1995-03-15
    PRIOR FILING DATE: 1995-03-15
    PRIOR PILING DATE: 1992-08-14
    PRIOR FILING DATE: 1992-08-14
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13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
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Mismatches:
          Sequence 5, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/105,617
PRIOR PILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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Sequence 128, App
Sequence 12, Appl
Sequence 44315, A
Sequence 90, Appl
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCE: PF23.
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
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                                       ALIGNMENTS
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Match Length DB
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| cgn2_6/ptodata1/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata1/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata1/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata1/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata1/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata1/1/pubpaa/USO8_PUBCOMB.pep:*
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                     protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: 60/31,469
PRIOR PILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-6-15
PRIOR PAPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
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; Sequence 1333, Application US/10293418
; Sequence 1333, Application No. US20030223996A1
; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1333
LENGTH: 253
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KUCHERLAPATI, RAJU
APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS, HAVING HUMAN IG LOCI INCLUDING
; TITLE OF INVENTION: THEREFROM
; TITLE OF INVENTION: THEREFROM
; TITLE OF INVENTION: UNMBER: US/10/078,958
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT APPLICATION NUMBER: 08/759,620
; PRIOR APPLICATION NUMBER: 08/759,620
17
                                       26 GlydluSerPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
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                                                                                18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAA
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                                                                                                                                                                                                                                                                                   Sequence 118, Application US/10371942
| Publication No. US20030223994A1
| GENERAL INFORMATION:
| APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
| APPLICANT: Hoogenboom, Herricus Renerus Jacobus Mattheus
| TITLE OF INVENTION: MAC-PEPTIDE COMPLEX BINDING LIGANDS
| TITLE REPRENCE: 10280-034001
| CURRENT PELING DATE: 2003-02-20
| CURRENT FILING DATE: 2003-02-20
| PRIOR FILING DATE: 2002-02-20
| NUMBER OF SEQ ID NOS: 121
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 118
| LENGTH: 125
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ORGANISM: Homo sapiens
US-10-371-942-118
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Best Local Similarity:
Query Match:
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Mismatches:
Indels:
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Publication No. US20030039649A1
GENERAL INFORMATION
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-07-12
                                                                                                                                                                  Gaps:
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
                                                                                                                                                                                         DELETED2 (1-81) x US-10-078-958-2 (1-80)
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US-10-308-817-83
'Sequence 83, Application US/10308917
'Publication No. US20030219861A1
'GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LENGTH: 97
                                                                                                      0.00107
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; NUMBER OF SEQ ID NOS: 79; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 2
                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-078-958-2
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US-10-194-975-40
                                   LENGTH: 80
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Sequence 87, Application US/10032037B

Sequence 87, Application US/10032037B

Sequence 87, Application US/10032037B

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT PLILNG DATE: 2001-12-31

FRIOR APPLICATION NUMBER: 60/258,948

FRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

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SEQ ID NOS: 204

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Matches:
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Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 97
TYPE: PRT
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Sequence 87, Application US/1002998BB
Publication No. US20040001839A1
GENERAL INCORMATION:
APPLICANT: Bio-Technology General Corp.
                                                                                                                                                                                                                                                                                DELETED2 (1-81) x US-10-308-817-83 (1-97)
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US-10-308-817-83
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Pred. No.:
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Matches:
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Mismatches:
Indels:
              Sequence 83, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION UMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
: EBNGTH: 97
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CRGANISM: human
US-10-453-698-83
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       US-10-453-698-83
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Publication No. US20040002450A1

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: V17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: NOTETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

TITLE OF INVENTION WHORER: US/10/032,423A

CURRENT APPLICATION NUMBER: 00/258,948

PRIOR FILING DATE: 12/29/2000

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 97
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-032-423A-87
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US-10-029-988B-87
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Squence 87, Application US/10029926B
Publication No. UGS20040073011A1
GENERAL INFORMATION:
APPLICANT: HAGAY. et al.
APPLICANT: HAGAY. et al.
TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 10793/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT FILING DATE: 2001-12-31
PRIOR PILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
61
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RESULT 10

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Best Local Similarity:
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Matches:
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                   Sequence 4. Application US/10379392
| Sequence 4. Application US/10379392
| Publication No. US20040110226A1
| GENERAL INPORMATION:
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Desjarlais, John Rudolf
| APPLICANT: Marshall, Shannon Allcia
| APPLICANT: Dahiyat, Bassil I.
| TITLE OF INVENTION: ANTIBODY OPTIMIZATION
| FILE REFERENCE: A-71386-3 46307-236
| CURRENT APPLICATION NUMBER: US/10/379,392
| CURRENT FILING DATE: 2002-03-01
| PRIOR FILING DATE: 2002-03-01
| PRIOR FILING DATE: 2002-03-01
| PRIOR FILING DATE: 2002-05-29
| NUMBER OF SEQ ID NOS: 184
| SOFTWARE: PALENTIN VERSION 3.2
| SEQ ID NO 47
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Query Match:
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US-10-733-532-128
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Pred. No.:
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Pred. No.:
             US-10-379-392-47
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US-10-379-392-47
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US-09-864-761-44315

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Sequence 4415, Application US/09864761

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Sequence 4415, Application Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Construction Constructi
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Publication No. US20050058642A1

GENERAL INFORMATION:

APPLICANT: SALIBERT, Laurent J.

APPLICANT: YAN, Wei

TITLE OF INVENTION: ANTAGONISTS OF LDCAM AND METHODS OF USE

FILE REPERBYCE: 3467-A

CURRENT FILLING DATE: 2004-07-23

FRIOR APPLICATION NUMBER: 60/490,027

PRIOR APPLICATION NUMBER: 60/490,027

PRIOR APPLICATION NUMBER: 60/490,027

FRIOR PILLING DATE: 2003-07-25

NUMBER: OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.2

SEQ ID NO 12

LENGTH: 115
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US-10-898-408-12
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PEATURE:
COTAINISM: Homo sapiens
FEATURE:
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
US-09-864-761-44315
PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00667

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

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DELETED2 (1-81) x US-09-864-761-44315 (1-117)

Percent Similarity: Best Local Similarity:

Query Match: DB:

62 yrAsnProSerLeuLysSer 68 62 ACAACCCGTCTCTCAAGAGT 81 ઠે

Search completed: August 4, 2005, 20:23:29 Job time : 106.5 secs

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Sequence 716, App
Sequence 716, App
Sequence 7283, A
Sequence 1333, Ap
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Sequence 1333, Ap
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Sequence 111128,
Sequence 144795,
Sequence 111072,
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Sequence 69, Appl
Sequence 87, Appl
Sequence 78284, A
Sequence 11367,
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Sequence 126333,
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Sequence 118, App
Sequence 110, App
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US-09-791-537-36503
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; Sequence 89288, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
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Sequence 144795, Application Us/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER:
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER:
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: Us/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARES: Patentin version 3.0
LENGTH: 97
LENGTH: 97
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Sequence 111072. Application US/09791537

Sequence 111072. Application US/09791537

Sequence 111072. Application US/09791537

APPLICANT: Debe, Derer

APPLICANT: Denser, Joseph

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REPRENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT PILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 111072

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US-09-791-537-111072
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE DE INVENTION: TRREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: WETHODS OF USE THEREOF
TITLE OF INVENTION: WOMBER: US/09/791,537
CURRENT APPLICATION UNMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 11128
                 APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT RILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 89288
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13 LysLeuSerGluAspLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
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Conservative:
Mismatches:
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74.57%
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; ORGANISM: Homo sapiens
US-09-791-537-111128
                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
  Debe, Derek
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Query Match:
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US-09-791-537-89288
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Pred. No.:
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Sequence 78283, Application US/09791537

Sequence 78283, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Dabe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE:
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE:
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE:
TITLE OF INVENTION: 151/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78283
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Danser, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PAPLICATION NUMBER: US/09/791,537
SOFTWARE PARENTING
SEQ ID NOS: 153055
SEQ ID NO 22691
LENGTH: 105
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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GENERAL INCOMMAILON:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523ECT
CURRENT APPLICATION NUMBER: PCT/USO1/19110
CURRENT PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1333
LENGTH: 253
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; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                           Sequence 1333, Application PC/TUS0119110; GENERAL INFORMATION:
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PCT-US01-19110-1333
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Best Local Similarity:
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Best Local Similarity:
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Sequence 1333, Application US/09880748

GENERAL INFORMATION:

TILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PP523

CURRENT FILING DATE: 2001-66-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

WUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1333
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Matches:
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Matches:
Conservative:
Mismatches:
Indels:
FILE REFERENCE: PF523PCT2
CURRENT APPLICATION NUMBER: PCT/US02/36496
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1333
LENGTH: 253
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ORGANISM: Homo sapiens
US-09-880-748-1333
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ORGANISM: Homo sapiens
PCT-US02-36496-1333
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                                                          18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAA
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GENERAL INCURATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPRENCE: PF52322

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/297,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/216,248

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

SEQ ID NO 1333

1.ENGTH: 253
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US-09-791-537-110576
; Sequence 110576, Application US/09791537
; GENBRAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
                                                                                                                                                                                                                               ; Sequence 1333, Application US/10293418
; GENERAL INFORMATION:
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Query Match:
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US-10-293-418-1333
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Pred. No.:
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DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBF
DDS OF USE THEREOF
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| GlyGlySer----IleSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Dyax Corporation, et al.

TITLE OF INVENTION: WHC-PERTIDE COMPLEX BINDING LIGANDS

FILE REFERENCE: 10280-034W01

CURRENT APPLICATION WUMBER: PCT/US03/05128

CURRENT APPLICATION NUMBER: PCT/US03/05128

FRIOR APPLICATION NUMBER: US 60/358,994

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 118
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Matches:
Conservative:
Mismatches:
Indels:
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCT
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 110576
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                           3 GCCGAGTCAGGATATTAGCAGC------
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3 GGCGAGTCAGGATATTAGCAGC-----24
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72 TCTCAAGAGT 81
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64 rLeuLysSer 67
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US-10-371-942-118
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Title: Perfect score:

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Gypecies (man) (fragment)

Ig heavy chain V-IV region - human (fragment)

C;Species (man)

C;Species (man)

C;Species (man)

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C;Species (man)

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C;Species (man)

S;Timmers (man)

S;Timmers (man)

S;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob

A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob

A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob

A;Reference number: A49028; MUID:92008140; PMID:1915549

A;Status: Dreliminary

A;Molecule type: mRNA

A;Residues: 1-143 < TINA

A;Residues: 1-143 < TINA

A;Cross-references: GB:S64473; NID:9236906; PIDN:AAB20012.1; PID:9236907

A;Cross-references (man)

A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)

C;Superfamily: immunoglobulin (man)

C;Superfamily: immunoglobulin (man)

C;Superfamily: immunoglobulin (man)

C;Superfamily: immunoglobulin (man)

C;Superfamily: immunoglobulin (man)

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                                               S54906
S26904
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I72667
S30529
JH0428
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cgn2 1/USFTO spool pVNOLAM463-3B/runat 04082005 120454 19622/app_query.fasta_1.263
-Q=/Cgn2 1/USFTO spool pVNOLAM463-3B/runat 04082005 120454 19622/app_query.fasta_1.263
-DB=FIR -QFRT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOFCL=0 -TOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LLST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DOCALIGN=200 -THR SCORE=500 -MINIEN=0 -MAXLEN=200000000
-USFA-NOLAN463-3B @CGN 1 1 63 @runat 04082005 120454 19622 -NCUPu=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPENOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
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                                                                                                    August 4, 2005, 19:51:37; Search time 25 Seconds (without alignments) 623.485 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd
                                                                            protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1 CGGGCGAGTCAGGATATTAG.
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Database

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1001.6 1000.4 988.2 988.

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Result

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Page

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C;Accession: S37454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
Rimcintosh, R.S.; Tandon, N.; Weetman, A.P.
Sptember 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A;Reference number: 837453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                          S26806

Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: J-Jan.1995 #sequence_revision 13-Jan.1995 #text_change 20-Jun-2000
C;Accession: S26806
C;Accession: S26806
R;Weng, N.; Snyder, J. G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                     A;Cross-references: EMBL:214242; NID:937716; PIDN:CAA78611.1; PID:91335377 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin Pils-97/Domain: immunoglobulin homology <IMM>
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A,Status: preliminary
A,Modecule type: mRNA
A,Modecule type: mRNA
A,Residues: 1-106 <MCI>
A,COSS=references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: immunoglobulin
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                     Percent Similarity:
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A; Residues: 1-97 < WEN>
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$256898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898; S12420
G;Accession: S26898; S12420
G;Accession: S26898; S12420
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID: 93021117; PMID: 1404388
A;Reference number: S26885; MUID: 93021117; PMID: 1404388
A;Reference number: S26885; MUID: 93021117; PMID: 1404388
A;Reserreferences: EMBL: Z12363; MID: 932944; PIDN: CAA78233.1; PID: 9322945
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A;Residues: 1-37 <TON>
A;Residues: DNA
A;Reference number: S09421; MUID: 90059975; PMID: 2511001
A;Ritle: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID: 90059975; PMID: 2511001
A;Residues: Lanslation not shown
A;Residues: L-97 <SAN>
A;Cross-references: EMBL: X56364
A;Residues: 1-97 <SAN>
A;Cross-references: EMBL: X56364
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A;Reperimental source: (MH) 4.
C;Superfamily: immunoglobulin homology <IMM>
C;Keywords: heterotetramer: immunoglobulin homology <IMM>
F;15-97/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
R; Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A; Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A; Reserence number: S268005 #UID:92201299; PMID:1348029
A; Accession: S268005
A; Status: preliminary
A; Molacule type: DNA
A; Residues: 1-97 - WEN-
A; Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C; Superfamily: immunoglobulin homology cimannoglobulin homology
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F; 15-97/Domain: immunoglobulin homology <INM>
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13 LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 TyrTrpSerTrp1leArgGlnProProGlyLysGlyLeuGluTrp1leGlyGlulleAsn 52
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Conservative:
Mismatches:
Indels:
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A;Molecule type: mRNA
A;Residues: 1.140 <hRx.
A;Cross.references: EMBL.X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
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R;Harinarath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and l
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R;Grillot-Courvalin, C; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverme Bur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
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A;Residues: 15-111 <HAM>
A;Crosa-references: EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                           Length:
Matches:
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Mismatches:
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Conservative:
Mismatches:
Indels:
Gaps:
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A;Reference number: S78051
A;Accession: S78052
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                                                                                Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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847010
19 heavy chain V4.21-UniqueD-J5 region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 13.-Jan.1995 #sequence_revision 13.-Jan.1995 #text_change 23.-Jul-1999
C;Accession: 547010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A;Reference number: 547009
A;Accession: 547010
A;Status: preliminary
A;Molecule type: mRNA
A;Retus: preliminary
A;Molecule type: mRNA
A;Reserences: EMBL:235492; NID:9517254; PIDN:CAA84625.1; PID:9517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-122 < BAE>
A; Residues: 1-122 < BAE>
A; Residues: 1-122 < BAE>
A; Note: the authors translated the reading frame which extends to the stop codon; the A; Note: this sequence belongs to the VH II subgroup
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotecramer; immunoglobulin homology < IMM>
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13
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Matches:
Conservative:
Mismatches:
Indels:
Matches:
Conservative:
Mismatches:
Indels:
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59.38%
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65.62%
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                      Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap. A;Reference number: A92830; MUD:89235232; PMID:2497188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S26905
Ig heavy chain V region (DP-70 / 4.19) - human (fragment)
C;Species: Home sapiens (man)
C;Date: 22-Nov-1993 Heequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826905; 812419
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Organia V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||::
|Trp1leGlyGlu1leAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT
                                         A, Molecule type: mRNA
A, Readdues: 1-133 «RAT»
A; Readdues: 1-133 «RAT»
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 9-38 Region: framework 1
F; 9-38 Region: complementarity-determining 1
F; 44-57/Region: framework 2
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A;Residues: 1-97 <SAN>
A;Cross-references: UNIRROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
      A; Reference number: PS0341; MUID: 92171937; PMID:1540170
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Matches:
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B23746
B23746
G2 Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C; Accession: B3746
B; Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A; Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglance number: A23746; MUID:91131575; PMID:1993660
A; Recession: B23746
A; Retern : preliminary
A; Roblecule type: protein
A; Residues: 1-231 cLEO>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 140-209/Domain: immunoglobulin homology < TMM>
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Ig heavy chain V-D-J region (RAMOS) - human (fragment)

Ig heavy chain V-D-J region (RAMOS) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997

C;Accession: Ps0341

R;Ratech, H.

Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992

A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
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A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-140 cGRI>
A;Cross-references: GB:S39381; NID:9250899; PIDN:AAB22441.1; PID:9250900
A;Cross-references: GB:S39381; NID:9250909; PIDN:AAB22441.1; PID:9250900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keyworfa: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-97 < ESJ>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TON
A;Residues: 1-98 <TON
A;Residues: 1-98 <TON
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Recession: S12419
A;Recession: S12419
A;Status: preliminary; translation not shown
A;Redidues: 1-98 <SAN
A;Cross-references: EMBL:X56363
A;Cross-references: EMBL:X56363
A;Cross-references: EMBL:X563001in V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
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A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and patient.
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A; Residues: 18-115 < HAM>
A; Cross-references: EMBL:X54445
A; Note: the authors translated the codon GCA for residue 67 as Arg
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
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R; van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H submitted to the EMBL Data Library, November 1990
A;Reference number: $14474
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
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TISSUE-Hodgkin lymphoma;
Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
Tinguely M.L., Brauninger A.;
Submitted (MAY-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564425; CAD92032.1; -.
HSSP; P18532; IKCV.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-ONAR-2004 (TrEMBLrel. 26, Last annotation update)
Rearranged VH4-34 V gene segment (Fragment)
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Q90QT5
Q9QKY2
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HV47 MOUSE
Q99CA9
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Q90QV6
Q96KX8
Q6QJ60
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Q99CH3
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Q9IUT6
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AAH19235.2; -.
PIR; G34964; G34964.
HSSP; P01861; 1ADQ.
PEam; PP07654; C1-set; 4.
SMART; SM00409; IG; 2.
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595 AA; 65290 MW; 0D4B50776545714E CRC64;
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TISSUB-Lymph;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; MASCHILL, Schuler G.D., Manden L., Max S.L., Wang J., Haide R., Caninon G.M., Hong L., Stanger C., Brownerein M.J., Usdin T.B., Toshiyuki S., Carninon R.D., Mullahy S.J., Bosak S.K., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Yullalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Mathing M., Madan A., Yourgan, M., Madan A., Yourgan, M., Madan A., Youthman J., Schmutz J., Myers R.M., Schein J.E., Schnerch A., Schein J.E., Anderstiel A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse CDMA sequences.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                      05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Mismatches:
Indels:
                                                                                                                                    597 AA.
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Matches:
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
                                                                                                                                    PRT;
InterPro; IPR003599; IG.
InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF007654; C1-set; 4.
Pfam; PF0047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00400; IGc1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUN-2004) to the
EMBL; BC073767; AAH73767.1;
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65.62%
59.38%
70.14%
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altacher R.D., Colline F.S., Wagner L., Schaefer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Astachench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toolhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garriacia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Murinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
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Jones S.J., Marra M.A.,
Johes C.D.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; RECO12963; AAH02963.1; -.
HSSP; P01861; 1ADQ.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches:
Conservative:
Mismatches:
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; Cl-eet; 4.
SMART; SM00406; IGv; 1.
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Homo sapiens (Human).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017355; AAH17356.2; -.
PIR; S15590; S15590.
HSSP; P01861; IADQ.
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 625 AA; 68610 MW; P62FAB3ADE7ECBFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625
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                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Conservative:
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InterPro; IPR00110; Ig-11ke.
InterPro; IPR00110; Ig-21.
InterPro; IPR001359; Ig_C1.
InterPro; IPR0013596; Ig_WHC.
InterPro; IPR001596; Ig_W-
Pfam; PR07654; C1-8et; 4.
SMART; SM00407; IG; 2.
SMART; SM00407; IGC1; 4.
                                                                       78 yrAsnProSerLeuLysSer
62 ACAACCCGTCTCTCAAGAGT
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                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   IGHM protein.
Homo sapiens (Human)
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SEQUENCE FROM N.A.
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Best Local Similarity:
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Pred. No.:
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DELETED2 (1-81) x Q96AA6 (1-625)

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Indels: Gaps:

DELETED2 (1-81) x Q9BU10 (1-597)

Best Local Similarity:

Query Match: OB:

Percent Similarity:

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deleted2.rup

81

62 ACAACCCGTCTCTCAAGAGT

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RESULT 7
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MEDLINE=2218825; PubWed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
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A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A blatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A black B.J., Marra M.A.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC006180; AAH06180.1; -.
HSSP; P01861; IADO.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MC.
InterPro; IPR003596; Ig_w.
PF07654; C1-set; 4.
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128
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches:
Conservative:
Mismatches:
                                                                                                                                             597 AA
                                                                                                                                            PRT;
                                              81
                                                                62 ACAACCCGTCTCTCAAGAGT
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56.25%
65.86%
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                                                                                                                                            PRELIMINARY;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Best Local Similarity:
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DB:
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                                                                                                            RESULT 6
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TISSUE=Primary B-Cells;

WEDINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratusberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marushia K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Wolfly K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063384; AAH63384.1; -
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                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Mismatches:
Indels:
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PROSITE; PS00290; IG MHC; UNKNOWN
SEQUENCE 576 AA; 63363 MW; FBB
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InterPro; IPR003109; Ig-like.
InterPro; IPR003597; Ig-like.
InterPro; IPR003506; Ig-MHC.
InterPro; IPR003066; Ig-MHC.
InterPro; IPR003596; Ig v.
Pfam; PF007654; Cl-Bet; Z.
SMART; SM00409; IG; 1.
SMART; SM004009; IG; 1.
SMART; SM004007; IGC1; 3.
0.00377
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48.89%
46.67%
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TISSUE=Primary B-Cells;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                               GHD protein.
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                                                                                                                                                                                                                                                Q6P418;
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DELETED2 (1-81)  $\times$  Q6P4I8 (1-576)

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
NA MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
Nado A., Ishihara T., Mishimura Y., Watanabe T.;
Nado A., Ishihara T., Mishimura T.,
Trepeat sequence in 5' flanking region.";
Trepeat sequence in 5' flanking region.";
Trepeat sequence in 5' flanking region.";
NPTR, A02101; G1HUH2.
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NPTR, A021
                                 ------TGGTTAGCCGAAATCATAGTGGAAGCACCAACTACAACCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V-II region ARH-77. V segment. D segment. J segment. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16228 MW; 8D7FD52BB218171F CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-II region ARH-77 precursor.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00047; ig; 1. 2—NARRT; SM00406; IGV; 1. PROSITE; PS56835; IG LIKE; 1. Immunoglobulin V region; Signal.
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Q6GMX7;
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QGGMX7
ID QGGM
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TISSUE=Primary B.CEL18;

KRY STRUESPTIMENCY B.CEL18;

KRY STRUESPTIMENCY B.CEL18;

KRA STRUESPTIMENCY COllins F.S., Wagner L., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Fanlac M.R., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Fabrar A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Widdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rabas S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gau, L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marza M.A.; sailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marza M.A.; Shalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. and mouse CDNA sequences.;

T. and mouse CDNA sequences.;

T. and mouse CDNA sequences.;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hymo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strauberrand (UUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC073765; AAH73765.1; -.
InterPro; IPR001359; Ig. InterPro; IPR00110; Ig-like. InterPro; IPR001359; Ig.cl. InterPro; IPR001506; Ig_MHC. InterPro; IPR003596; Ig_V. PF007654; Cl-set; Z.
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Matches:
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Pram; PP00047; ig; 3.
SNART; SM00409; IG; 4.
SNART; SM00406; IG; 4.
PROSITE; PS06265; IG LIKE; 4.
PROSITE; PS06290; IG MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GlyGlySer----ileSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl
                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODLOGYYM19 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGHM protein.

Homo sapiens (Human).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                     Homo sapiens (human) (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUBE-primary B-Cells;
MEDLINE-2238825; Pubmed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX240300; CAD62627.1;
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR007356; Ig-v.
                                                                                                                                                                                                                                                                                                                                                Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7D1E2302410E4F8C CRC64;
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Last annotation update)
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Matches:
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Mismatches:
Indels:
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                risSUE=B cells;
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A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Dosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Jones A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukarwords (Mouse).
Eukaryots Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857, AAH11857.2;
PIR; S15590; 815590.
HSSP: P01820; 1G7J.
HSSP: P01820; 1G7J.
HIGEPRO; IPR001359; 1G.
InterPro; IPR001359; 1G.
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InterPro; IRR001409; 1G.
InterPro; IRR001409; 1G.
IRC0141; SM0A407; 1GG1; 4.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990A1
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                                                 MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A strachul S.F., Collins P.S., Wagner L., Schaefer C.F., Bhat N.K.,
A strachul S.F., Zeberg B. B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A pitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B pitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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R Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
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LysProSerGlnSerLeuSerLeuThrCysSerValThrGlyTyrSerIleThrSerGly
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EMBL; BC002091; AAH02091.1; -...
HSSP; PO1020; 1G7J.
InterPro; IPR00130; Ig-11ke.
InterPro; IPR001359; Ig-c1.
InterPro; IPR003595; Ig-c1.
InterPro; IPR003596; Ig-wHC.
InterPro; IPR003596; Ig-v.
Pfam; PF07654; C1-set; Z.
SWART; SW00406; IG-y, 1.
PROSITE; PS00239; IG_LIKE; 4.
PROSITE; PS00239; IG_LIKE; UNKNOWN_2.
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479 AA; 51992 MW; 768E39A138918892 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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D HV61 MOUSE STANDARD; PRT; 116 AA. AC P1852.

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGGGCGAGTCAGGATATTAGC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRALM-EMLX FVB/N; TISSUE-Mammary tumor;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELETED2 (1-81) x Q99M22 (1-479)
                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.513
76.30
37.04%
27.78%
54.50%
                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
SEQUENCE 47
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Pred. No.:
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-----AGCTGGTTAGC 32
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                                                                       STRAIN=BALB/CJ;
MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
 Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 yTyrlleHisTyrSerGlyAsnThrSerTyrAsnProSerLeuLysSer
                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 CGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCAAGAGT
                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region 1B43.
Framework-1.
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                                                                                                                                                                          PIR; JT0508; HVMSIB.
PDB; 1KCS; X-ray; H=19-116.
PDB; 1KCY, X-ray; H=19-116.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv. 1.
PROSTIE; PS50815; IG_LIKE; 1.
PROSTIE; PS50815; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
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Matches:
Conservative:
Mismatches:
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.517
75.70
56.76%
43.24%
54.07%
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53
67
84
116
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Best Local Similarity:
                                                            SEQUENCE FROM N.A.
                             NCBI_TaxID=10090
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04332101024449
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05-JUL-2004
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DISULFID
STRAND
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SEQUENCE
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DB:
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.dl.
InterPro; IPR003597; Ig.dl.
InterPro; IPR003597; Ig.dl.
InterPro; IPR003597; Ig.dl.
Emm; PF00654; Ig.dl.
PFam; PF00647; Ig.dl.
SWART; SM00409; IG; 2.
SWART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IC_LIKE; 4.
PROSITE; PS0290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ACAACCCGTCTCTCAAGAGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELETED2 (1-81) x Q6GMX6 (1-465)
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75.20
56.25%
50.00%
53.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
Strausberg R.;
       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                 SEQUENCE FROM N.A
                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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Q65211;
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DB:
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ID Q65ZI
AC Q65ZI
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178 SerGlyTyr-TrpAsnTrp11eArgly8PheProGlyAsnLysLeuAspTyrMetGlyTy 197
                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Anti-HIV-1 reverse transcriptase single-chain variable.
Mus musculus (Mouse).
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Matches:
Conservative:
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Indels:
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72.80
55.56%
44.44%
52.00%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=10090;
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Search completed: August 4, 2005, 20:04:46 Job time : 120 secs